Package ‘rcosmo’

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Version 1.1.2

Description Handling and Analysing Spherical, HEALPix and Cosmic Microwave Background data on a HEALPix grid.

Depends R (>= 3.4.0)

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areCompatibleCMBDFs

Check compatibility of CMBDataFrames

Description

Compare attributes to decide if two CMBDataFrames are compatible

Usage

areCompatibleCMBDFs(cmbdf1, cmbdf2, compare.pix = FALSE)
**Arguments**

- `cmbdf1`: A `CMBDataFrame`
- `cmbdf2`: A `CMBDataFrame`
- `compare.pix`: A boolean. If TRUE then cmbdf1 and cmbdf2 must share the same pixel indices to be considered compatible

**Details**

If the CMBDataFrames do not have compatible attributes then a message is printed indicating the attributes that do not match. To suppress this use the `suppressMessages` function.

**Examples**

```r
a <- CMBDataFrame(nside = 2, ordering = "ring", coords = "cartesian")
b <- CMBDataFrame(nside = 1, ordering = "nested", coords = "spherical")
areCompatibleCMBDFs(a, b)
suppressMessages(areCompatibleCMBDFs(a, b))
```

---

**as.CMBDataFrame**

**Convert objects to CMBDataFrame**

**Description**

Safely converts a `data.frame` to a CMBDataFrame. The rows of the data.frame are assumed to be in the HEALPix order given by `ordering`, and at the HEALPix resolution given by `nside`. Coordinates, if present, are assumed to correspond to HEALPix pixel centers. The coordinates must be named either x,y,z (cartesian) or theta, phi (spherical colatitude and longitude respectively). If `df` is a HPDataFrame then it is possible that `df` has attribute `healpixCentered = TRUE`, in which case `as.CMBDataFrame` will perform HEALPix centering of coordinates.

**Usage**

```r
as.CMBDataFrame(df, ordering, nside, spix, drop.coords = FALSE)
```

**Arguments**

- `df`: Any `data.frame` or HPDataFrame whose rows are in HEALPix order
- `ordering`: character string that specifies the ordering scheme ("ring" or "nested")
- `nside`: an integer $2^k$ that specifies the Nside (resolution) HEALPix parameter
- `spix`: an integer vector that specifies the HEALPix pixel index corresponding to each row of `df`. If `spix` is left blank and `df` is a `data.frame`, then `df` is assumed to contain data for every pixel at resolution parameter `nside` (the full sky). In other words, in this case, the number of rows of `df` must be equal to $12*\text{nside}^2$. However, if `spix` is left blank and `df` is a `CMBDataFrame`, then `spix` is set equal to `pix(df)`
drop.coords A logical. If \( df \) is a HPDataFrame then it is possible that \( df \) has attribute healpixCentered = TRUE, in which case \( \text{as.CMBDataFrame} \) will perform HEALPix centering of coordinates. If drop.coords = TRUE then this will be done by dropping existing coordinates entirely (quicker) to rely only on HEALPix pixel indices. Otherwise if drop.coords = FALSE this will be done by replacing existing coordinates with locations of HEALPix pixel centers.

Value

A CMBDataFrame

Examples

```r
## Example 1: Create df with no coords, then create CMBDataFrames cmbdf and
df2 with spherical coords

df <- data.frame(I=rnorm(12))
df

cmbdf <- as.CMBDataFrame(df,ordering= "ring", nsid=1)
summary(cmbdf)
pix(cmbdf)
coords(cmbdf)

df2 <- coords(cmbdf, new.coords = "spherical")
df2

## Example 2: Create CMBDataFrames for first 10 Healpix centers

df <- data.frame(I=rnorm(10))
df
cmbdf <- as.CMBDataFrame(df,ordering= "ring", nsid=2, spix=1:10)
summary(cmbdf)
pix(cmbdf)
```

---

assumedConvex Check if a CMBWindow is assumed convex.

Description

Initially any CMBWindow is not assumed convex. The assumedConvex attribute can be change for any CMBWindow.

Usage

```r
assumedConvex(win, assume.convex)
```
assumedUniquePix

Arguments

- win: a CMBWindow object
- assume.convex: optionally change the assumedConvex attribute to TRUE or FALSE

Examples

```r
win1 <- CMBWindow(theta = c(0, pi/2, pi/2), phi = c(0, 0, pi/2))
assumedConvex(win1)
win2 <- assumedConvex(win1, assume.convex = TRUE)
assumedConvex(win2)
assumedConvex(win1) <- TRUE
assumedConvex(win1)
```

assumedUniquePix: **Check if object was assumed to have unique HEALPix indices**

Description

The function checks object's attribute assumedUniquePix. The attribute is True if the object was assumed to have rows that correspond to unique HEALPix pixel indices.

Usage

```r
assumedUniquePix(obj)
```

Arguments

- obj: Any object.

Value

A boolean. This is TRUE if obj is a CMBDataFrame or a HPDataFrame whose rows were assumed to correspond to unique HEALPix pixel indices.

Examples

```r
hp1 <- HPDataFrame(I=rnorm(5), nside = 1, spix = c(1,1,2,2,3))
pix(hp1)
coords(hp1, new.coords = "cartesian")
assumedUniquePix(hp1)

sky <- CMBDataFrame(nside = 32, coords = "cartesian", ordering = "nested")
sky.s <- CMBDataFrame(sky, sample.size = 100)
hpdf <- HPDataFrame(sky.s, auto.spix = TRUE)
assumedUniquePix(hpdf)
```
baseNeighbours

*Return neighbours of base pixels*

**Description**

The base-resolution comprises twelve pixels. baseNeighbours returns a map from the base pixel index bp to the vector of base pixels that are neighbours of bp, in counterclockwise order of direction: S,SE,E,NE,N,NW,W,SW. The presence of -1 indicates that the corresponding direction is empty.

**Usage**

```r
baseNeighbours(bp)
```

**Arguments**

bp

The base pixel index

**Examples**

```r
## Return neighbours of base pixel 1
baseNeighbours(1)
```

```r
## There is no base pixel 14, so baseNeighbours returns NULL
baseNeighbours(14)
```

---

**cbind.CMBDataFrame**

*cbind for CMBDataFrames*

**Description**

Add a new column or columns (vector, matrix or data.frame) to a `CMBDataFrame`. Note that method dispatch occurs on the first argument. So, the CMBDataFrame must be the first argument.

**Usage**

```r
## S3 method for class 'CMBDataFrame'
cbind(..., deparse.level = 1)
```

**Arguments**

...  

(generalized) vectors or matrices. Columns to bind.

deparse.level

Integer controlling the construction of labels in the case of non-matrix-like arguments.
chi2CMB

Details

See the documentation for `cbind`

Examples

```r
cmbdf <- CMBDataFrame(nside = 1, ordering = "nested", coords = "spherical")
cmbdf2 <- cbind(cmbdf, myData = rep(1, 12))
cmbdf2
```

---

chi2CMB | Chi-squared statistic for two CMBWindows

Description

This function returns the empirical chi-squared statistic for intensities observations from two `CMBWindow` s of the specified `CMBDataFrame`. The function employs the function `chi2.empirical` and uses histogram counts of intensities for computations.

Usage

```r
chi2CMB(cmbdf, win1, win2, intensities = "I")
```

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>cmbdf</td>
<td>A <code>CMBDataFrame</code>.</td>
</tr>
<tr>
<td>win1</td>
<td>A <code>CMBWindow</code>.</td>
</tr>
<tr>
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</tr>
<tr>
<td>intensities</td>
<td>A <code>CMBDataFrame</code> column with measured values.</td>
</tr>
</tbody>
</table>

Value

Estimated Chi-squared statistic for observations in two `CMBWindows`. For small sample sizes and many zero counts Chi-squared statistic is inefficient.

References

`chi2.empirical`
Examples

```r
# Download the map first
# downloadCMBMap(foreground = "smica", nside = 1024)
# df <- CMBDataFrame("CMB_map_smica1024.fits")
# cmbdf <- sampleCMB(df, sample.size = 1000)
#
# win1 <- CMBWindow(theta = c(0, pi/2, pi/2), phi = c(0, 0, pi/2))
# win2 <- CMBWindow(theta = c(pi/2, pi, pi/2), phi = c(0, 0, pi/2))
# plot(win1)
# plot(win2, col="green")
#
# chi2CMB(cmbdf, win1, win2)
```

---

### children

**Return children of a pixel**

**Description**

Gives four pixels at resolution $j + 1$ that are contained in $p$, where $p$ is a pixel specified at resolution $j$ (notice it does not depend on $j$).

**Usage**

`children(p)`

**Arguments**

- `p`: A pixel index specified in nested order.

**Examples**

```r
children(11)
```

---

### CMBDat

**CMBDat class**

**Description**

The function `CMBDat` creates objects of class `CMBDat`. These are lists containing header information and other metadata as well as an element called data, whose columns may include, for example, the intensity (I), polarisation (Q, U), PMASK and TMASK. It also may contain an `mmap` object that points to the CMB map data table in the FITS file.
Usage

`CMBDat(filename, mmap = FALSE, spix)`

Arguments

- `filename`: The path to the fits file.
- `mmap`: A boolean indicating whether to use memory mapping.
- `spix`: The sample pixels (rows) to read from the FITS file binary data table (optional)

Value

A list containing header information and other metadata as well as an element called data where:
- If `mmap = FALSE` then a `data.frame` is included, named data, whose columns may include, for example, the intensity (I), polarisation (Q, U), PMASK and TMASK. If `mmap = TRUE` then a `mmap` object is returned that points to the CMB map data table in the FITS file.

Examples

```r
## Ensure you have a FITS file with the correct path
## before running the example:
## download a FITS file and use real data
# downloadCMBMap()
# cmbdat <- CMBDat("CMB_map_smica1024.fits", mmap = TRUE)
# class(cmbdat)
# str(cmbdat)

## View metadata
# cmbdat$header1
# cmbdat$header2
# cmbdat$resoln
# cmbdat$method
# cmbdat$coordsys
# cmbdat$nside
# cmbdat$hdr
```

Description

The function `CMBDataFrame` creates objects of class `CMBDataFrame`. These are a special type of `data.frame` that carry metadata about, e.g., the HEALPix ordering scheme, coordinate system, and nside parameter.
CMBDataFrame

Usage

CMBDataFrame(CMBData, coords, win, include.polar = FALSE, include.masks = FALSE, spix, sample.size, nside, ordering, I, ...)  

Arguments

CMBData Can be a string location of FITS file, another CMBDataFrame, a CMBDat object, a HPDataFrame or unspecified.

coords Can be "spherical," "cartesian", or unspecified (HEALPix only).

win optional CMBWindow object that specifies a spherical polygon within which to subset the full sky CMB data.

include.polar TRUE if polarisation data is required, otherwise FALSE.

include.masks TRUE if TMASK and PMASK are required, otherwise FALSE.

spix Optional vector of sample pixel indices, or a path to a file containing comma delimited sample pixel indices. The ordering scheme is given by ordering. If ordering is unspecified then CMBData must be either a CMBDataFrame or a FITS file and the ordering scheme is then assumed to match that of CMBData.

sample.size If a positive integer is given, a simple random sample of size equal to sample.size will be taken from CMBData. If spix is specified then sample.size must be unspecified.

nside Optionally specify the nside parameter manually nside=2^k (usually 1024 or 2048).

ordering Specifies the desired HEALPix ordering scheme ("ring" or "nested") for the output CMBDataFrame. If ordering is unspecified then the ordering scheme will be taken from the CMBData object. If ordering information cannot be found the default will be "nested". This parameter also specifies the ordering scheme of spix.

I A vector of intensities to be included if CMBData is unspecified. Note that length(I) must equal 12 * nside^2 if either spix or sample.size are unspecified.

... Optional names data columns of length nrow(CMBData) to add to the CMBDataFrame.

Value

A CMBDataFrame whose row.names attribute contains HEALPix indices.

Examples

## Method 1: Read the data while constructing the CMBDataFrame
## download a FITS file and use real data
# downloadCMBMap()
# df <- CMBDataFrame("CMB_map_smica1024.fits")
df <- CMBDataFrame(nside = 16, I = rnorm(12 * 16 ^ 2), ordering = "nested")
# Specify a sample size for a random sample
df.sample <- CMBDataFrame(df, sample.size = 80)
plot(df.sample)

# Specify a vector of pixel indices using spix
df.subset <- CMBDataFrame(df, spix = c(2,4,6))

# Take a look at the summary
summary(df)

# Access HEALPix pixel indices using pix function
# (these are stored in the row.names attribute)
pix(df.subset)

---

**CMBWindow**

**CMBWindow class.**

**Description**

The function `CMBWindow` creates objects of class `CMBWindow`. It is either a polygon or a disc type.

**Usage**

`CMBWindow(..., r, set.minus = FALSE, assume.convex = FALSE)`

**Arguments**

- `...` these arguments are compulsory and must be labelled either x, y, z (cartesian) or theta, phi (spherical, colatitude and longitude respectively). Alternatively, a single data.frame may be passed in with columns labelled x, y, z or theta, phi.
- `r` if a disc type window is required then this specifies the radius of the disc
- `set.minus` when `TRUE` the window will be the unit sphere minus the window specified
- `assume.convex` when `TRUE` the window is assumed to be convex resulting in a faster computation time when the window is used with functions such as `subWindow`. This argument is irrelevant when the window is not a polygon

**Details**

If `r` is unspecified then the rows of `...` correspond to counter-clockwise ordered vertices defining a spherical polygon lying entirely within one open hemisphere on the unit sphere. Counter-clockwise is understood from the perspective outside the sphere, facing the hemisphere that contains the polygon, looking toward the origin. Note that there must be at least 3 rows (vertices) to define a polygon (we exclude bygones). On the other hand, if `r` is specified then `...` must specify just one row, and this row is taken to be the center of a disc of radius `r`
Examples

```r
win <- CMBWindow(theta = c(pi/2,pi/2,pi/3, pi/3), phi = c(0,pi/3,pi/3,0))
plot(win)

## Create a disc type window
win1<- CMBWindow(x=0,y=3/5,z=4/5,r=0.8, set.minus =TRUE)
plot(win1)

## Apply a disc type window to CMBDataFrame
cmbdf <- CMBDataFrame(nside = 64, coords = "cartesian", ordering = "nested")
window(cmbdf) <- CMBWindow(x=0,y=3/5,z=4/5,r=0.8, set.minus =TRUE)
plot(cmbdf)
```

coords.CMBDataFrame

**Description**

Detailed descriptions and examples can be found in documentation for specific coords functions `coords.CMBDataFrame, coords.CMBWindow, coords.HPDataFrame, coords.data.frame`

**Usage**

```r
coords(x, ...)
```

**Arguments**

- `x` An object.
- `...` Unused arguments.

**See Also**

`coords.CMBDataFrame coords.CMBWindow coords.HPDataFrame coords.data.frame`

```
 coords.CMBDataFrame    Coordinate system from a CMBDataFrame
```

**Description**

If `new.coords` is unspecified then this function returns the coordinate system used in the CMBDataFrame `cmbdf`. The coordinate system is either "cartesian" or "spherical". If a new coordinate system is specified, using e.g. `new.coords = "spherical"`, then this function instead returns a new CMBDataFrame whose coordinates are of the specified type. The original CMBDataFrame, `cmbdf`, is unaffected. If you would like to change `cmbdf` without creating a new variable, then use `coords<-`.CMBDataFrame` (see examples below).
## coords.CMBWindow

**Description**

This function returns the coordinate system used in a CMBWindow. The coordinate system is either "cartesian" or "spherical".

**Usage**

```r
## S3 method for class 'CMBDataFrame'
coords(x, new.coords, ...)
```

**Arguments**

- `x` A CMBDataFrame, cmbdf.
- `new.coords` Specifies the new coordinate system ("spherical" or "cartesian") if a change of coordinate system is desired.
- `...` Unused arguments.

**Value**

If `new.coords` is unspecified, then the name of the coordinate system of cmbdf is returned. Otherwise a new CMBDataFrame is returned equivalent to cmbdf but having the desired change of coordinates.

**Examples**

```r
## Create df with no coords, then create df2 with cartesian coords
df <- CMBDataFrame(nside = 16)
df
coords(df)
df2 <- coords(df, new.coords = "cartesian")
coords(df2)

## Change the coords of df directly (to spherical)
coords(df) <- "spherical"
coords(df)
```
## Arguments

- **x**: a `CMBWindow`, `win`.
- **new.coords**: specifies the new coordinate system ("spherical" or "cartesian") if a change of coordinate system is desired.
- **...**: Unused arguments.

## Details

If a new coordinate system is specified, using e.g. `new.coords = "spherical"`, the coordinate system of the `CMBWindow` will be converted.

## Value

If `new.coords` is unspecified, then the name of the coordinate system of `win` is returned. Otherwise a new `CMBWindow` is returned equivalent to `win` but having the desired change of coordinates.

## Examples

```r
## Create win with spherical coords, then change it to win1 with cartesian coords
win <- CMBWindow(theta = c(0, pi/2, pi/2), phi = c(0, 0, pi/2))
coords(win)
win1 <- coords(win, new.coords = "cartesian")
coords(win1)

## Change back to spherical coordinates
coords(win1) <- "spherical"
coords(win1)
```

---

### coords.data.frame

**Create a new data.frame with a given coordinate system**

## Description

This does not affect the original object unless new coordinate system is directly assigned.

## Usage

```r
## S3 method for class 'data.frame'
coords(x, new.coords, ...)
```

## Arguments

- **x**: a `data.frame` with columns labelled `x`, `y`, `z` (for cartesian) or `theta`, `phi` (for spherical colatitude and longitude respectively).
- **new.coords**: specifies the new coordinate system ("spherical" or "cartesian").
- **...**: Unused arguments.
Value

A new data.frame whose coordinates are as specified by new.coords

Examples

```r
## Create df with no coords, then create df2 with spherical coords
df <- data.frame(x = c(1,0,0), y = c(0,1,0), z = c(0,0,1))
df

df2 <- coords(df, new.coords = "spherical")
df2

## The function coords does not affect the original object.
## To change the coords assign a new value ("spherical" or "cartesian")
coords(df, new.coords = "spherical")
df
coords(df) <- "spherical"
df
```

coords.\texttt{HPDataFrame} \hspace{1cm} \textit{Coordinate system from a \texttt{HPDataFrame}}

Description

Add or change coordinates in a HPDataFrame. This does not affect the argument object \texttt{hpdf}. Instead it returns a new \texttt{HPDataFrame} with the desired coordinates. To change \texttt{hpdf} directly see \texttt{coords<-}.\texttt{HPDataFrame}.

Usage

```r
## S3 method for class 'HPDataFrame'
coords(x, new.coords, healpixCentered = FALSE, ...)
```

Arguments

- \texttt{x} \hspace{1cm} \texttt{a HPDataFrame, hpdf}.
- \texttt{new.coords} \hspace{1cm} \texttt{specifies the new coordinate system ("spherical" or "cartesian")}
- \texttt{healpixCentered} \hspace{1cm} \texttt{boolean. If TRUE then columns x,y,z or theta, phi will be ignored and removed if present. This forces the coordinates to be found from HEALPix pixel indices only. Then the HEALPixCentered attribute of \texttt{hpdf} will be set to TRUE.}
- \texttt{...} \hspace{1cm} \texttt{Unused arguments.}
Details

If columns exist labelled x,y,z (cartesian) or theta, phi (colatitude and longitude respectively), then these will be treated as the coordinates of hpdf and converted accordingly. If columns x,y,z or theta,phi are not present then the healpix pixel indices as given by pix(hpdf) are used for assigning coordinates.

Value

A HPDataFrame with columns x,y,z (cartesian) or theta, phi (colatitude and longitude respectively)

Examples

df <- HPDataFrame(I = rep(0,12), nside = 1)
coords(df, new.coords = "cartesian")
  # Notice that df is unchanged
  df

  # Instead, change df directly
  coords(df) <- "spherical"

  ## specify cartesian coordinates then convert to spherical
  hp1 <- HPDataFrame(x = c(1,0,0), y = c(0,1,0), z = c(0,0,1),
         nside = 1, auto.spix = TRUE)
  hp1 <- coords(hp1, new.coords = "spherical")

  ## Instead, ignore/drop existing coordinates and use HEALPix only
  hp2 <- HPDataFrame(x = c(1,0,0), y = c(0,1,0), z = c(0,0,1),
         nside = 1, auto.spix = TRUE)
  hp2 <- coords(hp1, new.coords = "spherical", healpixCentered = TRUE)
corrCMB

Arguments

cmbdf is a CMBDataFrame or data.frame
num.bins specifies the number of bins
sample.size optionally specify the size of a simple random sample to take before calculating
correlation. This may be useful if the full correlation computation is too slow.
max.dist an optional number between 0 and pi specifying the maximum geodesic distance
to use for calculating correlation. Only used if breaks are unspecified.
breaks optionally specify the breaks manually using a vector giving the break points
between cells. This vector has length num.bins since the last break point is
taken as max.dist. If equiareal = TRUE then these breaks should be \( \cos(r_i) \)
where \( r_i \) are radii. If equiareal = FALSE then these breaks should be \( r_i \).
equiareal if TRUE then the bins have equal spherical area. If false then the bins have equal
annular widths. Default is TRUE.
calc.max.dist if TRUE then the max.dist will be calculated from the locations in cmbdf.
Otherwise either max.dist must be specified or max.dist will default to pi.

Value

#' An object of the class CMBCorrelation that is a modification of variog from the package geoR
with variogram values replaced by correlation.
The attribute "breaks" contains the break points used to create bins. The result has num.bins + 1
values since the first value at distance 0 is not counted as a bin.

u a vector with distances.
v a vector with estimated correlation values at distances given in u.
n number of pairs in each bin
sd standard deviation of the values in each bin
bins.lim limits defining the interval spanned by each bin
ind.bin a logical vector indicating whether the number of pairs in each bin is greater or equal to
the value in the argument pairs.min
var.mark variance of the data
beta.ols parameters of the mean part of the model fitted by ordinary least squares
output.type echoes the option argument
max.dist maximum distance between pairs allowed in the correlation calculations
n.data number of data
direction direction for which the correlation was computed
call the function call

References

geoR package, variog, variogramCMB, covCMB
## Download the map first
```r
# downloadCMBMap(foreground = "smica", nside = 1024)
# df <- CMBDataFrame("CMB_map_smica1024.fits")
# cmbdf <- sampleCMB(df, sample.size = 100000)
# corcmb <- corrCMB(cmbdf, max.dist = 0.03, num.bins = 10, sample.size=1000)
# corcmb
```

---

### covCMB

#### Sample covariance function

**Description**

This function provides an empirical covariance function for data in a `CMBDataFrame` or `data.frame`. It assumes that data are from a stationary spherical random field and the covariance depends only on a geodesic distance between locations. Output is a binned covariance.

**Usage**

```r
covCMB(cmbdf, num.bins = 10, sample.size, max.dist = pi, breaks,
       equiareal = TRUE, calc.max.dist = FALSE)
```

**Arguments**

- `cmbdf` is a `CMBDataFrame` or `data.frame`
- `num.bins` specifies the number of bins
- `sample.size` optionally specify the size of a simple random sample to take before calculating covariance. This may be useful if the full covariance computation is too slow.
- `max.dist` an optional number between 0 and pi specifying the maximum geodesic distance to use for calculating covariance. Only used if `breaks` are unspecified.
- `breaks` optionally specify the breaks manually using a vector giving the break points between cells. This vector has length `num.bins` since the last break point is taken as `max.dist`. If `equiareal = TRUE` then these breaks should be $\cos(r_i)$ where $r_i$ are radii. If `equiareal = FALSE` then these breaks should be $r_i$.
- `equiareal` if TRUE then the bins have equal spherical area. If false then the bins have equal annular widths. Default is TRUE.
- `calc.max.dist` if TRUE then the `max.dist` will be calculated from the locations in `cmbdf`. Otherwise either `max.dist` must be specified or `max.dist` will default to pi.
Value

An object of the class CMBCovariance that is a modification of variog from the package geoR with variogram values replaced by covariances.

The attribute "breaks" contains the break points used to create bins. The result has num.bins + 1 values since the first value, the sample variance, is not counted as a bin.

u a vector with distances.
v a vector with estimated covariance values at distances given in u.
n number of pairs in each bin
sd standard deviation of the values in each bin
bins.lim limits defining the interval spanned by each bin
ind.bin a logical vector indicating whether the number of pairs in each bin is greater or equal to the value in the argument pairs.min
var.mark variance of the data
beta.ols parameters of the mean part of the model fitted by ordinary least squares
output.type echoes the option argument
max.dist maximum distance between pairs allowed in the covariance calculations
n.data number of data
direction direction for which the covariance was computed
call the function call

References

geoR package, variog, variogramCMB, corrCMB

Examples

```r
## Download the map first
# downloadCMBMap(foreground = "smica", nside = 1024)
# df <- CMBDataFrame("CMB_map_smica1024.fits")
# cmbdf <- sampleCMB(df, sample.size = 100000)
# Cov <- covCMB(cmbdf, max.dist = 0.03, num.bins = 10)
# Cov
```

Description

This function computes the covariances given the separation distance of locations. Options for different covariance functions on spheres are available. The function extends the function cov.spatial for additional covariance models on spheres.
Usage

covmodelCMB(obj, cov.model = "matern",
    cov.pars = stop("no cov.pars argument provided"), kappa = 0.5)

Arguments

obj Vector of distances between pairs of spatial locations.
cov.model A type of the correlation function. Available choices are: "matern", "exponential", "spherical", "powered.exponential", "cauchy", "gencauchy", "pure.nugget", "askey", "c2wendland", "c4wendland", "sinepower", "multiquadric". Default is "matern"
cov.pars A vector with two covariance parameters. The first parameter corresponds to the variance $\sigma^2$. The second parameter corresponds to the range $\phi$ of the correlation function.
kappa A smoothness parameter of the correlation function.

Details

The function returns the value of the covariance $C(h)$ at the distance $h$. The covariance function has the form

$$C(h) = \sigma^2 \cdot \rho(h/\phi).$$

The parameters of the covariance are positive numbers $\sigma^2$, $\phi$ and $\kappa$.

Expressions for the correlation functions which are not included in the package geoR:

askey

$$\rho(h/\phi) = (1 - h/\phi)^{\kappa}, \text{if } h < \phi;$$

$$0, \text{otherwise.}$$

c2wendland

$$\rho(h/\phi) = (1 + \kappa h/\phi) \cdot (1 - h/\phi)^{\kappa}, \text{if } h < \phi;$$

$$0, \text{otherwise.}$$

c4wendland

$$\rho(h/\phi) = (1 + \kappa h/\phi + (\kappa^2 - 1) \cdot h/\phi^2/3) \cdot (1 - h/\phi)^{\kappa}, \text{if } h < \phi;$$

$$0, \text{otherwise.}$$

sinepower

$$\rho(h/\phi) = 1 - (\sin(h/(2\phi)))^{\kappa}$$

multiquadric

$$C(h) = (1 - \phi^{(2\kappa)})/(1 + \phi^2 - 2 \cdot \phi \cdot \cos(h))^{\kappa}, 0 < \phi < 1$$

Additional information can be found in the section Details in cov.spatial.
Value

Values of a covariance function for the given distances.

References

geoR package, cov.spatial

Examples

## Compute Askey variogram at x = pi/4
1 - covmodelCMB(pi/4, cov.pars = c(1, pi), kappa = 3, cov.model = "askey")

## Plot of the Askey covariance function
v1.f <- function(x, ...) {covmodelCMB(x, ...)}
curve( v1.f(x, cov.pars = c(1, 0.03), kappa = 3, cov.model = "askey"),
from = 0, to = 0.1, xlab = "distance", ylab = expression(cov(h)), lty = 2,
main = "covariance")

covPwSp

Covariance estimate via power spectra

Description

This function provides a covariance estimate using the values of the estimated power spectra.

Usage

covPwSp(PowerSpectra, Ns)

Arguments

PowerSpectra A data frame which first column lists values of multipole moments and the second column gives the corresponding values of CMB power spectra.

Ns A number of points in which the covariance estimate is computed on the interval [-1,1]

Value

A data frame which first column is 1-d grid starting at -1+1/Ns and finishing at 1 with the step 2/Ns. The second column is the values of estimated covariances on this grid.
References


Power Spectra data are from Planck Legacy Archive http://pla.esac.esa.int/pla/#cosmology

Examples

```r
# Download the power spectrum first
N <- 20000
COM_PowerSpectra <- downloadCMBPS(link=1)

# Cov_est <- covPwSp(COM_PowerSpectra[,1:2], N)
# plot(Cov_est, type="l")

## Plot the covariance estimate as a function of angular distances
# plot(acos(Cov_est[,1]), Cov_est[,2], type ="l",
# xlab ="angular distance", ylab ="Estimated Covariance")
```

displayPixelBoundaries

*Plot HEALPix pixel boundaries*

Description

Plot the HEALPix pixel boundaries at nside

Usage

displayPixelBoundaries(nside, eps = pi/90, col = "gray", lwd = 1,
ordering, incl.labels = 1:(12 * nside^2), nums.col = col,
nums.size = 1, font = 2, depth_test = "always", ...)

Arguments

- `nside` the HEALPix nside parameter (integer number $2^k$
- `eps` controls the smoothness of the plot, smaller eps implies more samples
- `col` the colour of plotted boundary lines
- `lwd` the thickness of the plotted boundary lines
- `ordering` optionally specify an ordering scheme from which to plot HEALPix pixel numbers. Can be either "ring" or "nested"
- `incl.labels` If ordering is specified then this parameter sets the pixel indices that will be displayed (default is all indices at nside)
- `nums.col` specifies the colour of pixel numbers if ordering is specified
displayPixels

nums.size specifies the size of pixel numbers if ordering is specified
font A numeric font number from 1 to 5, used if ordering is specified
depth_test The depth test to be applied. This controls how resistant the plotted object is to being obscured. See rgl.material

... arguments passed to rgl::plot3d

Value

Produces a plot of the HEALPix pixel boundaries.

Examples

displayPixelBoundaries(1, eps = pi/90, col = "red")
displayPixelBoundaries(2, eps = pi/90, col = "green")

---

displayPixels

Display the pixels and grandchildren

Description

Display the pixels spix at resolution j by colouring in the grandchildren of spix at resolution plot.j

Usage

displayPixels(boundary.j, j, plot.j = 5, spix, boundary.col = "gray",
boundary.lwd = 1, incl.labels = 1:(12 * 4^boundary.j),
col = "blue", size = 3)

Arguments

boundary.j The resolution to display boundaries at. If this is missing then boundaries will not be plotted.
j The resolution that spix are specified at.
plot.j The resolution to plot grandchildren at
spix Integer vector. The pixel indices to display. These must be in nested order.
boundary.col The boundary colour.
boundary.lwd The boundary line width.
incl.labels Integer vector of pixel indices to label at resolution j.
col The colour to make the grandchildren.
size The size to make the grandchildren.
Examples

```r
## Example 1

## Plot base pixels 1,2,3 by colouring their grandchildren at resolution 5 (by default). No pixel boundaries.
displayPixels(j=0, spix=c(1,2,3))

## Plot base pixels 1,2,3 display and their boundaries (boundary.j=0)
displayPixels(0,0, spix=c(1,2,3))

## Plot base pixels 1,2,3 by colouring their grandchildren at resolution 2
displayPixels(0,0, plot.j = 2, spix=c(1,2,3))

## Example 2
demoNeighbours <- function(p,j) {
  neighbours(p, j)
  displayPixels(boundary.j = j, j = j, plot.j = 5,
    spix = neighbours(p, j),
    boundary.col = "gray",
    boundary.lwd = 1,
    incl.labels = neighbours(p, j),
    col = "blue",
    size = 3)
  rcosmo::displayPixelBoundaries(nside = 1, col = "blue", lwd = 3)
}
demoNeighbours(1,2)
```

downloadCMBMap

Download CMB Maps from Planck Public Data Release.

Description

The function `downloadCMBMap` downloads CMB maps from [http://irsa.ipac.caltech.edu/data/Planck/release_2/all-sky-maps/matrix_cmb.html](http://irsa.ipac.caltech.edu/data/Planck/release_2/all-sky-maps/matrix_cmb.html).

Usage

`downloadCMBMap(foreground = "smica", nside = 1024, destfile)`

Arguments

- **foreground**: A string naming the foreground separation method pipeline. Please choose one of "COMMANDER", "NILC", "SEVEM" or "SMICA" (not case sensitive).
- **nside**: An integer. The nside parameter (resolution) required. The available options are 1024 or 2048.
downloadCMBPS

`downloadCMBPS` downloads CMB Power Spectra from Planck Legacy Archive.

**Description**

The function `downloadCMBPS` downloads CMB power spectra components from [http://pla.esac.esa.int/pla/#cosmology](http://pla.esac.esa.int/pla/#cosmology).

**Details**

CMB maps have been produced by the COMMANDER, NILC, SEVEM, and SMICA pipelines, respectively.

For each pipeline, the intensity maps are provided at Nside = 2048, at 5 arcmin resolution, and the polarization maps are provided at Nside = 1024 at 10 arcmin resolution.

**Value**

CMB Map FITS File (Flexible Image Transport System). The FITS file can be loaded into a `CMBDataFrame` using the `CMBDataFrame` function (see examples).

**References**

Planck Public Data Release 2 Maps [http://irsa.ipac.caltech.edu/data/Planck/release_2/all-sky-maps/matrix_cmb.html](http://irsa.ipac.caltech.edu/data/Planck/release_2/all-sky-maps/matrix_cmb.html)

Other fits maps can also be downloaded using the general command `download.file`.

**Examples**

```r
## Download SMICA with `nside = 1024`
## and save in working directory
## as "CMB_map_smica1024.fits"
# downloadCMBMap(foreground = "smica", nside = 1024)
## Load the downloaded map into a CMBDataFrame
# sky <- CMBDataFrame("CMB_map_smica1024.fits")

## Download SMICA with Nside=2048 and save in the working directory
## as "CMB_map_smica2048.fits"
# downloadCMBMap(foreground = "smica", nside = 2048)

## Download COMMANDER with Nside=1024 and save in a specified folder,
## for example,
# dest <- "CMB_map_commander1024.fits"
# downloadCMBMap(foreground = "commander", nside = 1024, destfile = dest)
```
downloadCMBPS

Usage

downloadCMBPS(link = 1, destfile, save = TRUE)

Arguments

link The link code (an integer from 1 to 6) for the URL to download the file. See code details in this help file.

destfile A character string with the file name for the downloaded file to be saved. Tilde-
expansion is performed.

save A boolean indicating whether to save or not (since the downloaded data is returned anyway).

Details

link = 1: Best-fit LCDM CMB power spectra from the baseline Planck TT, TE, EE+lowE+lensing
(2 <= ell <= 2508).
link = 2: Baseline high-ell Planck TT power spectra (2 <= ell <= 2508).
link = 3: Baseline high-ell Planck EE power spectra (2 <= ell <= 1996).
link = 4: Baseline high-ell Planck TE power spectra (2 <= ell <= 1996).
link = 5: Low-ell Planck EB power spectra (2 <= ell <= 29).
link = 6: Low-ell Planck BB power spectra (2 <= ell <= 29).

Value

The Data Frame with CMB Power Spectra and, if save = TRUE a txt file is saved in destfile.

References

Planck Legacy Archive http://pla.esac.esa.int/pla/#cosmology

Examples

## Download the Low-ell Planck BB power spectra (2 <= ell <= 29) and
## save it to C:/PW.txt
# downloadCMBPS(link=6, destfile="C:/PW.txt")

## Download the Best-fit LCDM CMB power spectra
## and plot it
# CMBPS <- downloadCMBPS(link=1, save = FALSE)
# plot(CMBPS$L,CMBPS$TT, type="o",col="red",cex=0.3,
# main="CMB Angular Power Spectra",xlab=expression(l),
# ylab=expression(paste(D[l],"(",mu,K^2,",")")))
entropyCMB

CMB Entropy

Description

This function returns an estimated entropy for the specified `CMBDataFrame` column intensities and `CMBWindow` region. The function employs the function `entropy` and uses histogram counts of intensities for computations. All arguments of the standard `entropy` can be used.

Usage

```r
entropyCMB(cmbdf, win, intensities = "I", method)
```

Arguments

- **cmbdf**: A `CMBDataFrame`.
- **win**: A `CMBWindow`
- **intensities**: A `CMBDataFrame` column with measured values.
- **method**: A method to estimate entropy, see `entropy`

Value

Estimated Shannon entropy for observations in `CMBWindow`

References

`entropy`

Examples

```r
## Download the map first
# downloadCMBMap(foreground = "smica", nside = 1024)
# df <- CMBDataFrame("CMB_map_smica1024.fits")
# cmbdf <- sampleCMB(df, sample.size = 10000)
# win1 <- CMBWindow(theta = c(0,pi/2,pi/2), phi = c(0,0,pi/2))
# entropyCMB(cmbdf, win1)
```
exprob  

Threshold exceedance probability

Description
This function returns an estimated exceedance probability for the specified `CMBDataFrame` column intensities, threshold level \( \alpha \) and `CMBWindow` region.

Usage

\[
\text{exprob}(\text{cmbdf}, \text{win}, \alpha, \text{intensities} = "I")
\]

Arguments

- `cmbdf`  
  A `CMBDataFrame`.  
- `win`  
  A `CMBWindow`.  
- `alpha`  
  A numeric threshold level.  
- `intensities`  
  The name of the column in `cmbdf` that contains the measured values.

Value

Estimated threshold exceedance probability

Examples

```r
## Download the map first
# downloadCMBMap(foreground = "smica", nside = 1024)
# df <- CMBDataFrame("CMB_map_smica1024.fits")
# cmbdf <- sampleCMB(df, sample.size = 1000)

# intensities <- "I"
# alpha <- mean(cmbdf[,intensities, drop = TRUE])
# alpha

# win1 <- CMBWindow(theta = c(0,pi/2,pi/2), phi = c(0,0,pi/2))
# exprob(cmbdf, win1, alpha)
```
extrCMB

Extreme values

Description

This function returns \( n \) largest extreme values for the specified \texttt{CMBDataFrame} column \texttt{intensities} and \texttt{CMBWindow} region.

Usage

\[
\text{extrCMB(cmbdf, win, n, intensities = "I")}
\]

Arguments

- \texttt{cmbdf} A \texttt{CMBDataFrame}.
- \texttt{win} A \texttt{CMBWindow}
- \texttt{n} An integer value.
- \texttt{intensities} A \texttt{CMBDataFrame} column with measured values.

Value

A \texttt{CMBDataFrame} with \( n \) largest extreme values

Examples

```r
## Download the map first
# downloadCMBMap(foreground = "smica", nside = 1024)
# df <- CMBDataFrame("CMB_map_smica1024.fits")
# cmbdf <- sampleCMB(df, sample.size = 1000)
#
# win1 <- CMBWindow(theta = c(pi/2,pi,pi/2), phi = c(0,0,pi/2))
# extrCMB(cmbdf, win1,5)
#
## Ploting the window and 5 top extreme values
# plot(win1)
# plot(extrCMB(cmbdf, win1,5), col ="blue", size = 4,add = TRUE)
```
Description

This function returns an area of the spherical region where measured values are above of the specified threshold level \( \alpha \).

Usage

\[
\text{fmf}(\text{cmbdf, alpha, intensities = "I"})
\]

Arguments

\[
\begin{align*}
\text{cmbdf} & \quad \text{A \texttt{CMBDataFrame}.} \\
\text{alpha} & \quad \text{A numeric threshold level.} \\
\text{intensities} & \quad \text{A \texttt{CMBDataFrame} column with measured values.}
\end{align*}
\]

Value

The area of the exceedance region

References


Examples

\[
\begin{align*}
n & \leftarrow 64 \\
cmbdf & \leftarrow \text{CMBDataFrame}(\text{nside}=n, I = \text{rnorm}(12*n^2), \\
& \text{coords = "cartesian",} \\
& \text{ordering = "nested"}) \\
\text{fmf}(\text{cmbdf, 0, 4}) \\
\text{fmf}(\text{cmbdf, 2, 4}) \\
\text{win} & \leftarrow \text{CMBWindow}(\text{theta = c(0,pi/2,pi/2), phi = c(0,0,pi/2))} \\
cmbdf\text{.win} & \leftarrow \text{window(cmbdf, new.window = win)} \\
\text{fmf}(\text{cmbdf\text{.win, 0, 4})}
\end{align*}
\]
Sample Renyi function

Description

This function computes values of the sample Renyi function. Returns the estimated values of \( T(q) \) for \( q \) taking values on a grid. For large data sets could be rather time consuming.

Usage

\[
fRen(cmbdf, q.min = 1.01, q.max = 10, N = 20, k.box = \log_2(\text{nside}(cmbdf)) - 3, \text{intensities} = "I")
\]

Arguments

- \( cmbdf \): A \texttt{CMBDataFrame}.
- \( q.min \): Left endpoint of the interval to compute the Renyi function. The default value is 1.01.
- \( q.max \): Right endpoint of the interval to compute the Renyi function. The default value is 10.
- \( N \): Number of points to compute the Renyi function. The default value is 20.
- \( k.box \): A dyadic decomposition level in computing the Renyi function, see the references in Details. The default value is \( \log_2(\text{nside}(cmbdf)) - 3 \).
- \( \text{intensities} \): A \texttt{CMBDataFrame} column with measured values.

Value

Data frame which first column is the sampling grid \( \text{seq}(q.min, q.max, \text{length.out} = N) \) of \( q \) values. Another column consists of values of the sample Renyi function \( T(q) \) computed on the grid using the \( k.box \)th level dyadic decomposition of the unit ball.

References


Examples

```r
## Download the map first
# downloadCMBMap(foreground = "smica", nside = 1024)
#
# cmbdf <- CMBDataFrame("CMB_map_smica1024.fits")
# win <- CMBWindow(theta = c(pi/4, pi/2, pi/2), phi = c(0,0,pi/2))
# cmbdf <- window(cmbdf, new.window = win)
```
# Tq <- fRen(cmbdf)
#
# plot(Tq[,1], Tq[,2], ylab = expression(D[q]), xlab = "q",
# main = "Sample Renyi function", pch = 20, col = "blue")

geo2sph

*Convert geographic to spherical coordinates*

**Description**

Convert latitude (lat) and longitude (lon) to spherical coordinates (theta, phi) with theta in $[0, \pi]$ and phi in $[0, 2\pi]$. All values lat, lon, theta, phi are assumed to be in radians.

**Usage**

```r
geo2sph(...)```

**Arguments**

... A data.frame with columns lat and lon, or named vectors of lat and lon.

**Value**

A data.frame with columns theta and phi.

**Examples**

```r
geo <- data.frame( lat = c(0, pi/3, pi/2), lon = c(0, pi/3, pi))
geo
sph <- geo2sph(geo)
sph
```

geoAngle

*Angle between two spherical directions*

**Description**

Get an angle between two directions defined by arcs on the unit sphere.

**Usage**

```r
geoAngle(p1)```
Arguments

p1 A `data.frame` with rows specifying numeric points located on the unit sphere. It should have columns labelled x,y,z for Cartesian or theta, phi for spherical colatitude and longitude respectively.

Value

Let $p1[1,], p1[2,]$, and $p1[3,]$ denote the rows of p1. Then the returned object is an angle in radians between two arcs determined by the pairs of spherical points $(p1[1,], p1[2,])$ and $(p1[2,], p1[3,])$ respectively.

Examples

```r
p1 <- data.frame(diag(3))
p1
colnames(p1) <- c("x", "y", "z")
geoAngle(p1)

geo <- data.frame(lat = c(30, 0, 20), lon = c(30, 60, 10))*(pi/180)
geo
p2 <- geo2sph(geo)
p2
geoAngle(p2)
```

---

geoArea generic

Description

Detailed descriptions and examples can be found in documentation for specific geoArea functions `geoArea.CMBDataFrame`, `geoArea.HPDataFrame`, `geoArea.CMBWindow`

Usage

`geoArea(x)`

Arguments

x An object.

See Also

`geoArea.CMBDataFrame`, `geoArea.HPDataFrame`, `geoArea.CMBWindow`
geoArea.CMBDataFrame  Geodesic area covered by a CMBDataFrame

Description

Gives the surface on the unit sphere that is encompassed by all pixels in cmbdf

Usage

## S3 method for class 'CMBDataFrame'
geoArea(x)

Arguments

x  a CMBDataFrame.

Value

The sum of the areas of all pixels (rows) in x.

Examples

## At low resolution, a few data points can
## occupy a large pixel area, e.g.:

cmbdf <- CMBDataFrame(nside = 1, spix = c(1,2,3))
pix(cmbdf)

## The total number of Healpix points at nside=1 equals 12. As cmbdf has 3 Healpix
## it occupies \pi = \frac{1}{4\pi} (surface area of unit sphere)

geoArea(cmbdf)
plot(cmbdf, size = 5, hp.boundaries = 1)

geoArea.CMBWindow  Geodesic area of a CMBWindow

Description

Geodesic area of a CMBWindow

Usage

## S3 method for class 'CMBWindow'
geoArea(x)
geoArea.HPDataFrame

Arguments

x A CMBWindow.

Value

The spherical area inside the CMBWindow x.

Examples

```r
## A window that covers 1/8 of the unit sphere is constructed and its area is
## pi/2 = 1/8*(surface area of unit sphere)
win <- CMBWindow(theta = c(0, pi/2, pi/2), phi = c(0, 0, pi/2))
geoArea(win)
```

geoArea.HPDataFrame  

Geodesic area covered by a HPDataFrame

Description

Gives the surface on the unit sphere that is encompassed by all pixels in x.

Usage

```r
## S3 method for class 'HPDataFrame'
geoArea(x)
```

Arguments

x A HPDataFrame.

Value

The sum of the areas of all pixels (rows) in x.

Examples

```r
## Generate random I for HPDataFrame
hp1 <- HPDataFrame(I=rnorm(5), nside = 1, spix = c(1,1,2,2,3))
pix(hp1)

## The total number of Healpix points at nside=1 equals 12. As hp1 has five
## I values at 3 Healpix points, then the occupied area is
## pi = 1/4*(surface area of unit sphere)
geoArea(hp1)
```
```r
plot(hp1, size = 5, hp.boundaries = 1)
```

---

**geoDist**

*Geodesic distance on the unit sphere*

**Description**

Get geodesic distance between points on the unit sphere

**Usage**

```r
geoDist(p1, p2, include.names = FALSE)
```

**Arguments**

- **p1**
  - A `data.frame` with rows specifying numeric points located on the unit sphere. It should have columns labelled x,y,z for Cartesian or theta, phi for spherical colatitude and longitude respectively.
- **p2**
  - Same as p1.
- **include.names**
  - Boolean. If TRUE then the row and column names of the returned matrix will be taken from the points in `p1` and `p2` (see examples below).

**Value**

Let \( n \) denote the number of rows of \( p1 \) and let \( m \) denote the number of rows of \( p2 \). Then the returned object is an \( n \) by \( m \) matrix whose entry in position \( ij \) is the geodesic distance from the \( i \)th row of \( p1 \) to the \( j \)th row of \( p2 \).

**Examples**

```r
p1 <- data.frame(diag(3))
colnames(p1) <- c("x", "y", "z")
p1
p2 <- data.frame(x=c(1,0), y=c(0,3/5), z=c(0,4/5))
p2
geoDist(p1, p2, include.names = FALSE)
```
header  

Get the FITS headers from a CMBDataFrame

Description
Get the FITS headers from a CMBDataFrame

Usage
header(cmbdf)

Arguments

cmbdf a CMBDataFrame.

Value
The FITS headers belonging to the FITS file from which cmbdf data was imported

Examples
## First download the map
# downloadCMBMap(foreground = "smica", nside = 1024)
# df <- CMBDataFrame("CMB_map_smica1024.fits")
# df.sample <- CMBDataFrame(df, sample.size = 10000)
# header(df.sample)

healpixCentered  

Check if object is assumed to have HEALPix centered coordinates

Description
The function checks object's attribute healpixCentered. The attribute is TRUE if the object was assumed to have rows that correspond to unique HEALPix pixel indices.

Usage
healpixCentered(obj)

Arguments
obj Any object.

Value
A boolean. This is TRUE if obj is a CMBDataFrame or a HPDataFrame whose coordinates were assumed to correspond to HEALPix pixel center locations.
Examples

```r
hp1 <- HPDataFrame(I=rnorm(5), nside = 1, spix = c(1,1,2,2,3))
pix(hp1)
coords(hp1, new.coords = "cartesian")
healpixCentered(hp1)

sky <- CMBDataFrame(nside = 32, coords = "cartesian", ordering = "nested")
sky.s <- CMBDataFrame(sky, sample.size = 100)
hpdf <- HPDataFrame(sky.s, auto.spix = TRUE)
healpixCentered(hpdf)
```

---

**HPDataFrame**

**HPDataFrame class**

**Description**

HPDataFrames are a type of `data.frame` designed to carry data located on the unit sphere. Each row of a HPDataFrame is associated with a HEALPix pixel index. The HPDataFrame also holds an attribute called `nside` which stores the HEALPix Nside parameter (i.e., the resolution of the HEALPix grid that is being used). Unlike `CMBDataFrame`, HPDataFrames may have repeated pixel indices. They are made this way so that multiple data points falling within a given pixel can be stored in different rows of any given HPDataFrame.

**Usage**

```r
HPDataFrame(..., nside, ordering = "nested", auto.spix = FALSE, spix,
assumedUniquePix = FALSE, delete.duplicates = FALSE,
save.dots = FALSE, save.duplicate.indices = FALSE)
```

**Arguments**

- `...` Data. Can be named vectors or a `data.frame`. May include columns (x,y,z) or (theta, phi) representing Cartesian or spherical coordinates of points on the unit sphere.
- `nside` Integer number $2^k$, the nside parameter, i.e, resolution. If `nside` is unspecified, then the an attempt is made to use columns x,y and z from the provided data, as Cartesian coordinates, to calculate an nside that is sufficient to ensure all points belong to unique pixels.
- `ordering` The HEALPix ordering scheme ("ring" or "nested").
- `auto.spix` Boolean. If TRUE then spix will be found from the coordinates provided in the data. That is, each row of data will be assigned the pixel index of its closest HEALPix pixel center. There must be columns x,y,z for cartesian or theta, phi for spherical colatitude and longitude respectively. If `auto.spix` = FALSE then `nside` must be specified.
spix A vector of HEALPix pixel indices indicating the pixel locations of the data. Note that spix is ignored if auto.spix = TRUE.

assumedUniquePix A boolean. Sets the assumedUniquePix attribute of the HPDataFrame. This attribute indicates whether or not the rows of a HPDataFrame can be assumed to belong to unique pixels.

delete.duplicates Boolean. If TRUE then rows corresponding to duplicate pixel indices will be dropped from the returned HPDataFrame, and assumedUniquePix will be set to TRUE.

save.dots A logical. If TRUE then the dot product of each observation with the nearest child HEALPix pixel center will be stored as a column called "distance" in the returned HPDataFrame, provided that auto.spix = TRUE. Note that a 'child' pixel is any one of the four pixels contained in the current pixel, in the nested scheme, at the next highest resolution. See children.

save.duplicate.indices A logical. If TRUE and delete.duplicates is also TRUE, then the row indices of duplicated pixels will be retained as an attribute called "duplicates". Note that row index refers to the row position of the duplicated pixel in the original HPDataFrame, and not the actual pixel index itself.

Details

HPDataFrame with auto.spix = TRUE can be used to transform any spherical data (not necessarily CMB) to the Healpix representation, see Example 3 below.

Examples

##Example 1.

hp1 <- HPDataFrame(I=rnorm(5), nside = 1, spix = c(1,1,2,2,3))
pix(hp1)
coords(hp1, new.coords = "cartesian")
class(hp1)
assumedUniquePix(hp1)

##Example 2.

# Where nside is not specified
sky <- CMBDataFrame(nside = 32, coords = "cartesian", ordering = "nested")

sky.s <- CMBDataFrame(sky, sample.size = 100)

hpdf <- HPDataFrame(sky.s, auto.spix = TRUE)
class(hpdf)
assumedUniquePix(hpdf)

# ## Example 3.
# ## Create a HPDataFrame with NON-UNIQUE pixel indices
#
With earth data.
Download World Cities Database from
https://simplemaps.com/static/data/world-cities/basic/simplemaps_worldcities_basicv1.4.zip
unpack the file worldcities.csv

worldcities <- read.csv("worldcities.csv")

Prepare a data frame with cities' coordinates
sph <- geo2sph(data.frame(lon = pi/180*worldcities$lng,
lat = pi/180*worldcities$lat))
df <- data.frame(phi = sph$phi,
theta = sph$theta,
I = rep(1,nrow(sph)))

Create and plot the corresponding HPDataFrame with
pixel indices that are not necessarily unique
by choosing your desired resolution \(nside\)
hp <- HPDataFrame(usdf, auto.spix = TRUE, nside = 1024)
plot(hp, size = 3, col = "darkgreen", back.col = "white")
Add some pixels to visualise the sphere
plot(CMBDataFrame(nside = 64), add = TRUE, col = "gray")

Example 4.
Create a HPDataFrame with UNIQUE pixel indices.

With earth data.
Download World Cities Database from
https://simplemaps.com/static/data/world-cities/basic/simplemaps_worldcities_basicv1.4.zip
unpack the file worldcities.csv

worldcities <- read.csv("worldcities.csv")
uscities <- worldcities[worldcities$country == "United States",]

Prepare a data frame with cities' coordinates
sph <- geo2sph(data.frame(lon = pi/180*uscities$lng,
lat = pi/180*uscities$lat))
usdf <- data.frame(phi = sph$phi,
theta = sph$theta,
I = rep(1,nrow(sph)))

Select \(k\) cities with unique coordinates. The
coordinates must be unique otherwise the
automatically chosen separating \(nside\)
will be infinite.
k <- 1000
usdf <- usdf[sample(nrow(usdf), k),]
plot(usdf$phi, usdf$theta)
usdf[duplicated(usdf),]
usdf <- usdf[!duplicated(usdf),]
usdf[duplicated(usdf),]
usdf <- coords(usdf, new.coords = "cartesian")

Create and plot the corresponding HPDataFrame. To make
ibp2p

Computes pixel’s index using its subindex within base resolution

Description

Find the pixel index \( p \) of a given pixel with index \( ibp \) in base pixel \( bp \).

Usage

ibp2p(ibp, bp, j)

Arguments

ibp The pixel index within base pixel \( bp \), at resolution \( j \), in nested order.
bp The base pixel index
j The resolution parameter \( \text{nside} = 2^j \)

Examples

ibp2p(1, 1, 2)
ibp2p(1, 2, 2)

is.CMBDat

Check if an object is of class CMBDat

Description

Check if an object is of class CMBDat

Usage

is.CMBDat(cmbdf)
is.CMBDataFrame

Check if an object is of class CMBDataFrame

Description

Check if an object is of class CMBDataFrame

Usage

is.CMBDataFrame(cmbdf)

Arguments

cmbdf  Any R object

Value

TRUE if cmbdf is a CMBDataFrame, otherwise FALSE

Examples

```r
df <- CMBDataFrame(nside = 16)
is.CMBDataFrame(df)
df2 <- coords(df, new.coords = "cartesian")
is.CMBDataFrame(df2)
```
is.CMBWindow

Description

Check if an object is a CMBWindow

Usage

is.CMBWindow(win)

Arguments

win any object

Value

TRUE or FALSE depending if win is a CMBWindow

Examples

win <- CMBWindow(x=0,y=3/5,z=4/5,r=0.8, set.minus = TRUE)
is.CMBWindow(win)

is.HPDataFrame

Description

Check if an object is of class HPDataFrame

Usage

is.HPDataFrame(hpdf)

Arguments

hpdf Any R object

Value

TRUE if hpdf is a HPDataFrame, otherwise FALSE
Examples

```r
df <- CMBDataFrame(nside = 16)
is.HPDataFrame(df)

df <- HPDataFrame(I = rep(0,12), nside = 1)
is.HPDataFrame(df)
```

---

**linesCMB**

*Adds lines of fitted variograms to variogram plots*

Description

This function adds a line with the variogram model fitted by the function `variofitCMB` to a current variogram plot. The function modifies `lines.variomodel.variofit` from the package `geoR` for additional covariance models on spheres.

Usage

```r
linesCMB(x, max.dist, scaled = FALSE, ...)
```

Arguments

- **x**: An object of the class `variofit` containing information about the fitted model obtained as an output of the function `variofitCMB`.
- **max.dist**: A maximum distance to draw the variogram line. The default is `x$max.dist`.
- **scaled**: logical. If TRUE the sill in the plot is 1.
- **...**: other plotting parameters passed to `curve`

Details

The function adds a line with fitted variogram model to a plot. It is used to compare empirical variograms against fitted models returned by `variofitCMB`.

Available models are: "matern", "exponential", "spherical", "powered.exponential", "cauchy", "gen-cauchy", "pure.nugget", "askey", "c2wendland", "c4wendland", "sinepower", "multiquadric".

Value

A line with a fitted variogram model is added to a plot.

References

- `geoR` package, `lines.variomodel.variofit`, `covmodelCMB`, `variofitCMB`
Examples

```r
## Plot the fitted Matern variogram versus its empirical variogram
# df <- CMBDataFrame("../CMB_map_smica1024.fits")
# cmbdf <- sampleCMB(df, sample.size = 10000)
# varcmb <- variogramCMB(cmbdf, max.dist = 0.1, num.bins = 30)
# varcmb
# ols <- variofitCMB(varcmb, fix.nug=FALSE, wei="equal", cov.model="matern")
# plot(varcmb)
# lines(ols, lty=2)

## Plot the fitted Askey variogram versus its empirical variogram
# ols <- variofitCMB(vario1, ini.cov.pars = c(1, 0.03), fix.nug = TRUE,
# kappa = 3, wei = "equal", cov.model = "askey")
# plot(varcmb, main = ols$cov.model)
# linesCMB(ols, lty = 2)
```

maxDist

*Get the maximum geodesic distance between points*

**Description**

Get the maximum geodesic distance either between all points in a data.frame pairwise, or between all points in a data.frame and one target point.

**Usage**

```r
maxDist(df, point)
```

**Arguments**

- `df` A data.frame with columns x,y,z for cartesian or theta, phi for spherical colatitude and longitude respectively. The rows must correspond to points on the unit sphere. If this is a HPDataFrame or CMBDataFrame and coordinate columns are missing, then coordinates will be assigned based on HEALPix pixel indices.
- `point` An optional target point on the unit sphere in cartesian coordinates, in which case all distances are calculated between point and the points in df.

**Value**

If point is specified: the longest geodesic distance from point to the points specified by the rows of df. If point is not specified: the longest geodesic distance pairwise between points in df.
Examples

```r
## Using a CMBDataFrame with HEALPix coordinates only
cmbdf <- CMBDataFrame(nside = 1, spix = c(1,5,12), ordering = "ring")
plot(cmbdf, hp.boundaries = 1, col = "blue", size = 5)
p <- c(0,0,1)
maxDist(cmbdf, p) # no need to have coordinates

## Using a HPDataFrame with HEALPix coordinates only
hp <- HPDataFrame(nside = 1, I = rep(0,3), spix = c(1,5,12) )
maxDist(hp, p) # notice no need to have coordinates

## Using a data.frame with cartesian coordinates
coords(hp) <- "cartesian"
df <- data.frame(x = hp$x, y = hp$y, z = hp$z)
maxDist(df, p)

## Using a data.frame with spherical coordinates
coords(hp) <- "spherical"
df <- data.frame(theta = hp$theta, phi = hp$phi)
maxDist(df, p)

## max distance between points in cmdf
maxDist(cmbdf)
```

maxWindowDist

Get the maximum distance between all points in a CMBWindow

Description

Get the maximum distance between all points in a CMBWindow

Usage

maxWindowDist(x)

Arguments

x A CMBWindow object.

Value

The maximum distance between window's points.
Examples

```r
## win is a equilateral spherical triangle which sides are pi/2
win <- CMBWindow(theta = c(0,pi/2,pi/2), phi = c(0,0,pi/2))
maxWindowDist(win)
```

---

`minDist`  
*Get the minimum geodesic distance between points*

Description

Get the minimum geodesic distance either between all points in a data.frame pairwise, or between all points in a data.frame and one target point.

Usage

`minDist(df, point)`

Arguments

- `df`: A data.frame with columns x,y,z for cartesian or theta, phi for spherical colatitude and longitude respectively. The rows must correspond to points on the unit sphere. If this is a `HPDataFrame` or `CMBDataFrame` and coordinate columns are missing, then coordinates will be assigned based on HEALPix pixel indices.
- `point`: An optional target point on the unit sphere in cartesian coordinates, in which case all distances are calculated between point and the points in `df`.

Value

If `point` is specified: the shortest distance from `point` to the points specified by the rows of `df`. If `point` is not specified: the shortest distance pairwise between points in `df`.

Examples

```r
## Using a CMBDataFrame with HEALPix coordinates only
cmbdf <- CMBDataFrame(nside = 1, spix = c(1,5,12), ordering = "ring")
plot(cmbdf, hp.boundaries = 1, col = "blue", size = 5)
p <- c(0,0,1)
minDist(cmbdf, p) # no need to have coordinates

## Using a HPDataFrame with HEALPix coordinates only
hp <- HPDataFrame(nside = 1, l = rep(0,3), spix = c(1,5,12) )
minDist(hp, p) # notice no need to have coordinates

## Using a data.frame with cartesian coordinates
coords(hp) <- "cartesian"
```
df <- data.frame(x = hp$x, y = hp$y, z = hp$z)
minDist(df, p)

## Using a data.frame with spherical coordinates
coords(hp) <- "spherical"
df <- data.frame(theta = hp$theta, phi = hp$phi)
minDist(df, p)

## min distance between points in cmdf
minDist(cmbdf)

---

**neighbours**

*Return neighbouring pixels*

**Description**

Return the neighbouring pixels to a given pixel `p` that is specified at resolution `j`, in the nested order.

**Usage**

```r
neighbours(p, j)
```

**Arguments**

- `p`: Pixel index `p` at resolution `j`.
- `j`: The resolution parameter with `nside = 2^j`.

**Examples**

```r
## Return the neighbouring pixels for base pixel 1
neighbours(1, 0)

## Plot the neighbouring pixels for base pixel 1
demoNeighbours <- function(p,j) {
  neighbours(p, j)
  displayPixels(boundary.j = j, j = j, plot.j = j+3,
               spix = neighbours(p, j),
               boundary.col = "gray",
               boundary.lwd = 1,
               incl.labels = neighbours(p, j),
               col = "blue",
               size = 3)
  rcosmo::displayPixelBoundaries(nside = 1, col = "blue", lwd = 3)
}
demoNeighbours(1,2)
demoNeighbours(1,0)
```
**nest2ring**  
*Convert nest to ring ordering*

**Description**
Convert from "nested" to "ring" ordering

nest2ring computes the HEALPix pixel index in the "ring" ordering scheme from the pixel index in the "nested" ordering scheme.

**Usage**

```r
nest2ring(nside, pix)
```

**Arguments**

- `nside` is the HEALPix nside parameter.
- `pix` is the set or subset of pixel indices at nside. If pix is left blank then all pixels are converted.

**Value**
the output is the corresponding set of pixel in the ring ordering scheme.

**Examples**

```r
# compute HEALPix indices in the ring ordering scheme
nside <- 8
pix <- c(1,2,23)
nest2ring(nside, pix)
```

**nestSearch**  
*Finds the closest pixel center to a point*

**Description**
Finds the closest HEALPix pixel center to a given target point, specified in Cartesian coordinates, using an efficient nested search algorithm. HEALPix indices are all assumed to be in the "nested" ordering scheme.

**Usage**

```r
nestSearch(target, nside, index.only = FALSE, save.dots = FALSE)
```
Arguments

**target**
A data.frame, matrix or vector of Cartesian (x,y,z) coordinates for the target point. If a data.frame is used then spherical coordinates can be specified with row names theta and phi.

**nside**
An integer, the target resolution at which the resulting pixels are returned.

**index.only**
A boolean indicating whether to return only the pixel index (TRUE), or cartesian coordinates as well (FALSE).

**save.dots**
A logical. A If TRUE then the dot product of each observation with the nearest child HEALPix pixel center will be returned as an attribute called "dot". Note that a 'child' pixel is any one of the four pixels contained in the current pixel in the nested scheme, at the next highest resolution. See children.

Value

If index.only = TRUE then the output will be a HEALPix index. If index.only FALSE then the output is the list containing the HEALPix index and Cartesian coordinate vector of the HEALPix point closest to target at resolution nside.

Examples

```r
## Find the closest HEALPix pixel center at resolution j=2 for
## the point (0.6,0.8,0)
point <- c(0.6,0.8,0)
j <- 2
cpoint <- nestSearch(point, nside = 2^j)

## Plot the closest pixel center in blue and the point (0.6,0.8,0) in red
displayPixels(j, j, plot.j=j, spix=c(cpoint$pix),
size=5, incl.labels =FALSE)
rgl::plot3d(point[1], point[2], point[3],
col="red", size = 5, add = TRUE)

## Repeat the above for 4 points in a data.frame
points <- data.frame(x = c(1,0,0,0.6),
y = c(0,1,0,0.8),
z = c(0,0,1,0))

points
j <- 2
cpoints <- nestSearch(points, nside = 2^j)

## Plot the closest pixel center in blue and the point (0.6,0.8,0) in red
displayPixels(j, j, plot.j=j, spix=c(cpoints$pix),
size=5, incl.labels =FALSE)
rgl::plot3d(points[,1], points[,2], points[,3],
col="red", size = 5, add = TRUE)
```
Description

Detailed descriptions and examples can be found in documentation for specific nside functions
nside.CMBDataFrame, nside.HPDataFrame

Usage

nside(x)

Arguments

x An object.

See Also

nside.CMBDataFrame nside.HPDataFrame

nside.CMBDataFrame

**HEALPix Nside parameter from a CMBDataFrame**

Description

This function returns the HEALPix Nside parameter of a CMBDataFrame

Usage

```r
## S3 method for class 'CMBDataFrame'
nsided(x)
```

Arguments

x A CMBDataFrame.

Value

The HEALPix Nside parameter.

Examples

df <- CMBDataFrame(nside = 16)
nside(df)
numeric2col

Description
Map numeric values to a colour map

Usage
numeric2col(num, colmap = grDevices::terrain.colors(100),
  breaks.length = length(colmap))

Arguments
num  A numeric vector. The numbers which will be mapped to colours.
colmap A colour map. See palette.
breaks.length A single integer. Controls the number of breaks in the discretisation of num.
Examples

```r
ns <- 16
sky <- CMBDataFrame(I = rnorm(12*ns^2), nside = ns)
plot(sky, col = numeric2col(sky$I))
```

Description

Detailed descriptions and examples can be found in documentation for specific ordering functions `ordering.CMBDataFrame`, `ordering.HPDataFrame`.

Usage

```r
ordering(x, ...)
```

Arguments

- `x` An object.
- `...` Extra arguments.

See Also

- `ordering.CMBDataFrame`, `ordering.HPDataFrame`

ordering.CMBDataFrame

*HEALPix ordering scheme from a CMBDataFrame*

Description

This function returns the HEALPix ordering scheme from a CMBDataFrame. The ordering scheme is either "ring" or "nested".

Usage

```r
## S3 method for class 'CMBDataFrame'
ordering(x, new.ordering, ...)
```

Arguments

- `x` A `CMBDataFrame`.
- `new.ordering` Specifies the new ordering ("ring" or "nest") if a change of ordering scheme is desired.
- `...` Unused arguments.
ordering.HPDataFrame

Details

If a new ordering is specified, using e.g. new.ordering = "ring", the ordering scheme of the CMBDataFrame will be converted.

Value

The name of the HEALPix ordering scheme that is used in the CMBDataFrame x.

Examples

df <- CMBDataFrame(nside = 1, ordering = "nested")
ordering(df)

df1 <- ordering(df, new.ordering = "ring")
ordering(df1)

ordering.HPDataFrame

HEALPix ordering scheme from a HPDataFrame

Description

This function returns the HEALPix ordering scheme from a HPDataFrame. The ordering scheme is either "ring" or "nested". If a new ordering is specified, using e.g. new.ordering = "ring", the ordering scheme of the HPDataFrame will be converted.

Usage

## S3 method for class 'HPDataFrame'
ordering(x, new.ordering, ...)

Arguments

x a HPDataFrame.

new.ordering Specifies the new ordering ("ring" or "nest") if a change of ordering scheme is desired.

... Unused arguments.

Value

The name of the HEALPix ordering scheme that is used in the HPDataFrame x, or a new HPDataFrame with the desired new.ordering
**Examples**

```r
df <- HPDataFrame(I = rep(0,12), nside = 1, ordering = "nested")
ordering(df)
df1 <- ordering(df, new.ordering = "ring")
ordering(df1)
```

---

**p2bp**  
_Return base pixel to which pixel belongs_

**Description**

The base pixel to which pixel \( p \) belongs at resolution \( j \)

**Usage**

`p2bp(p, j)`

**Arguments**

- **p**  
The pixel index at resolution \( j \), in nested order.
- **j**  
The resolution parameter \( \text{nside} = 2^j \)

**Examples**

```r
p2bp(5, 0)
p2bp(5, 1)
```

---

**p2ibp**  
_Return pixel index within its base pixel_

**Description**

Convert a pixel index \( p \) to its index within the base pixel to which \( p \) belongs

**Usage**

`p2ibp(p, j)`

**Arguments**

- **p**  
The pixel index at resolution \( j \), in nested order.
- **j**  
The resolution parameter \( \text{nside} = 2^j \)
Examples

\[
\begin{align*}
p2ibp(6, 0) \\
p2ibp(6, 1)
\end{align*}
\]

\[
\begin{array}{ll}
\text{parent} & \text{Return index of parent pixel}
\end{array}
\]

Description

Gives the pixel at resolution \( j - 1 \) that contains \( p \), where \( p \) is specified at resolution \( j \) (notice it does not depend on \( j \)).

Usage

\[
\text{parent}(p)
\]

Arguments

\[
p \quad \text{A pixel index specified in nested order.}
\]

Examples

\[
\begin{align*}
\text{parent}(4) \\
\text{parent}(5)
\end{align*}
\]

\[
\begin{array}{ll}
pix & pix \ generic
\end{array}
\]

Description

Detailed descriptions and examples can be found in documentation for specific pix functions pix.CMBDataFrame,pix.HPDataFrame

Usage

\[
pix(x, \ldots)
\]

Arguments

\[
\begin{align*}
x & \quad \text{An object.} \\
\ldots & \quad \text{Extra arguments.}
\end{align*}
\]

See Also

pix.CMBDataFrame pix.HPDataFrame
Description

If new.pix is unspecified then this function returns the vector of HEALPix pixel indices from a CMBDataFrame. If new.pix is specified then this function returns a new CMBDataFrame with the same number of rows as cmbdf, but with pix attribute new.pix. Thus, new.pix must have length equal to nrow(cmbdf).

Usage

## S3 method for class 'CMBDataFrame'
pix(x, new.pix, ...)

Arguments

x         A CMBDataFrame.
new.pix   Optional vector of pixel indices with length equal to nrow(x).
...       Unused arguments.

Value

The vector of HEALPix pixel indices or, if new.pix is specified, a new CMBDataFrame.

Examples

## First download the map
# downloadCMBMap(foreground = "smica", nside = 1024)
# df <- CMBDataFrame("CMB_map_smica1024.fits", sample.size = 800000)
# pix(df)

df <- CMBDataFrame(nside = 16, sample.size = 10, ordering = "nested")
pix(df)

Description

If new.pix is unspecified then this function returns the vector of HEALPix pixel indices from a HPDataFrame. If new.pix is specified then this function returns a new HPDataFrame with the same number of rows as x, but with pix attribute new.pix. Thus, new.pix must have length equal to nrow(x).
Usage

```r
## S3 method for class 'HPDataFrame'
pix(x, new.pix, ...)
```

Arguments

- `x` a `HPDataFrame`.
- `new.pix` optional vector of pixel indices with length equal to `nrow(x)`
- `...` Unused arguments.

Value

The vector of HEALPix pixel indices (integers) or, if `new.pix` is specified, a new HPDataFrame.

Examples

```r
df <- HPDataFrame(I = rep(0,12), nside = 1)
pix(df)
```

---

**pix2coords**

Convert pixel indices to cartesian/spherical coordinates

Description

Convert HEALPix pixel indices to cartesian or spherical coordinates

Usage

```r
pix2coords(nside, coords = "cartesian", ordering = "nested", spix)
```

Arguments

- `nside` the `nside` parameter (integer number $2^k$)
- `coords` 'cartesian' or 'spherical' coordinates
- `ordering` 'ring' or 'nested' ordering
- `spix` optional integer or vector of sample pixel indices

Value

A data.frame with columns 'x', 'y', 'z' (cartesian) or 'theta', 'phi' (spherical)

Examples

```r
pix2coords(nside=1, spix=c(2,5))
pix2coords(nside=1, coords = "spherical", spix=c(2,5))
```
**pixelArea**

*Area of a HEALPix pixel*

**Description**

Get the area of a single HEALPix pixel

**Usage**

```r
pixelArea(nsideObject)
```

**Arguments**

- `nsideObject`  
  CMBDataFrame, a HPDataFrame, or an integer giving the nside parameter.

**Value**

the area of a single HEALPix pixel at the nside resolution of `nsideObject`

**Examples**

```r
## First download the map
# downloadCMBMap(foreground = "smica", nside = 1024)
# df <- CMBDataFrame("CMB_map_smica1024.fits")
# pixelArea(df)

df1 <- CMBDataFrame(nside = 64,
    coords = "cartesian",
    ordering = "nested")
pixelArea(df1)
```

---

**pixelWindow**

*Find high resolution pixels falling in a lower resolution window*

**Description**

Find all pixels in a higher resolution that fall within the specified pixel area at a lower resolution. All pixels are assumed to be in nested ordering.

**Usage**

```r
pixelWindow(j1, j2, pix.j1)
```
Arguments

- **j1** An integer. The lower resolution, with j1 <= j2.
- **j2** An integer. The upper resolution.
- **pix.j1** An integer. The pixel index at resolution j1 within which all pixels from resolution j2 will be returned. pix.j1 can also be a vector of non-zero pixel indices.

Value

All pixels in resolution j2 that fall within the pixel pix.j1 specified at resolution j1

Examples

```r
pixelWindow(3, 3, 2)
pixelWindow(3, 4, 2)
pixelWindow(3, 5, 2)
```

Description

Plots sample (empirical) correlation function. Uses `plot.variogram` from `geoR` package.

Usage

```r
## S3 method for class 'CMBCorrelation'
plot(x, ...)  
```

Arguments

- **x** An object of class CMBCorrelation.
- **...** Extra arguments as in `plot.variogram` passed to `plot.default`.

Value

Produces a plot with the sample correlation function.

References

`geoR` package, `corrCMB`, `variog`, `plot.variogram`
Examples

```r
## Download the map first
# downloadCMBMap(foreground = "smica", nside = 1024)
# df <- CMBDataFrame("CMB_map_smica1024.fits")
# cmbdf <- sampleCMB(df, sample.size = 100000)
# corcmbH <- corrCMB(cmbdf, max.dist = 0.03, num.bins = 10, sample.size=1000)
# plot(corcmbH)
```

---

**Description**

Plots sample (empirical) covariance function. Uses `plot.variogram` from `geoR` package.

**Usage**

```r
## S3 method for class 'CMBCovariance'
plot(x, ...)  
```

**Arguments**

- `x` An object of class CMBCovariance.
- `...` Extra arguments as in `plot.variogram` passed to `plot.default`.

**Value**

Produces a plot with the sample covariance function.

# @references `geoR` package, `covCMB`, `variog`, `plot.variogram`

**Examples**

```r
## Download the map first
# downloadCMBMap(foreground = "smica", nside = 1024)
# df <- CMBDataFrame("CMB_map_smica1024.fits")
# cmbdf <- sampleCMB(df, sample.size = 100000)
# Cov <- covCMB(cmbdf, max.dist = 0.03, num.bins = 10)
# plot(Cov)
```
plot.CMBDataFrame  

Plot CMB Data

Description

This function produces a plot from a CMBDataFrame.

Usage

```r
## S3 method for class 'CMBDataFrame'
plot(x, intensities = "I", add = FALSE,
     sample.size, type = "p", size = 1, box = FALSE, axes = FALSE,
     aspect = FALSE, col, back.col = "black", labels, hp.boundaries = 0,
     hpb.col = "gray", depth_test = "less", lab_depth_test = "always",
...)
```

Arguments

- **x**: A CMBDataFrame.
- **intensities**: The name of a column that specifies CMB intensities. This is only used if `col` is unspecified.
- **add**: If TRUE then this plot will be added to any existing plot. Note that if `back.col` (see below) is specified then a new plot window will be opened and `add = TRUE` will have no effect.
- **sample.size**: Optionally specifies the size of a simple random sample to take before plotting. This can make the plot less computationally intensive.
- **type**: A single character indicating the type of item to plot. Supported types are: 'p' for points, 's' for spheres, 'l' for lines, 'h' for line segments from z = 0, and 'n' for nothing.
- **size**: The size of plotted points.
- **box**: Whether to draw a box.
- **axes**: Whether to draw axes.
- **aspect**: Either a logical indicating whether to adjust the aspect ratio, or a new ratio.
- **col**: Specify the colour(s) of the plotted points.
- **back.col**: Optionally specifies the background colour of the plot. This argument is passed to rgl::bg3d.
- **labels**: Optionally specify a vector of labels to plot, such as words or vertex indices. If this is specified then rgl::text3d is used instead of rgl::plot3d. Then `length(labels)` must equal `nrow(x)`.
- **hp.boundaries**: Integer. If greater than 0 then HEALPix pixel boundaries at `nside = hp.boundaries` will be added to the plot.
- **hpb.col**: Colour for the hp.boundaries.
plot.CMBWindow

**depth_test**  The depth test to be applied to the plotted points. This controls how resistant the plotted object is to being obscured. See `rgl.material`.

**lab_depth_test**  The `rgl` depth test to be applied to the labels and pixel boundaries if present. See `rgl.material`.

...  Arguments passed to `rgl::plot3d`.

**Value**

A plot of the CMB data.

**Examples**

```r
## First download the map
# downloadCMBMap(foreground = "smica", nside = 1024)
# sky <- CMBDataFrame("CMB_map_smica1024.fits")
# plot(sky, sample.size = 800000)
```

**Description**

Visualise a CMBWindow.

**Usage**

```r
## S3 method for class 'CMBWindow'
plot(x, add = TRUE, type = "l", col = "red",
     size = 2, box = FALSE, axes = FALSE, aspect = FALSE, back.col,
     depth_test = "always", ...)
```

**Arguments**

- **x**  A CMBWindow.
- **add**  if TRUE then this plot will be added to any existing plot. Note that if back.col (see below) is specified then a new plot window will be opened and add = TRUE will have no effect.
- **type**  a single character indicating the type of item to plot. Supported types are: 'p' for points, 's' for spheres, 'l' for lines, 'h' for line segments from z = 0, and 'n' for nothing.
- **col**  specify the colour(s) of the plotted points
- **size**  the size of plotted points
- **box**  whether to draw a box
- **axes**  whether to draw axes
### plot.HPDataFrame

#### Description

This function produces a plot from a `HPDataFrame`. If columns `x,y,z` (cartesian) or `theta,phi` (colatitude and longitude respectively) are present in `x`, then these will be used as coordinates for plotting. Otherwise, the HEALPix indices as in `pix(x)` will be used. If HEALPix indices are used and multiple rows correspond to a single pixel index, then beware that values may be obfuscated in the plot, and all locations are pixel centers.

#### Usage

```r
## S3 method for class 'HPDataFrame'
plot(x, intensities = "I", add = FALSE, sample.size, type = "p", size = 1, box = FALSE, axes = FALSE, aspect = FALSE, col = "blue", back.col = "black", labels, hp.boundaries = 0, hpb.col = "gray", depth_test = "less", lab_depth_test = "always", ...)
```

#### Arguments

- **x**: A `HPDataFrame`.
- **intensities**: The column name for the data in `x` that is to be treated as intensities for plotting.
- **add**: if `TRUE` then this plot will be added to any existing plot. Note that if `back.col` (see below) is specified then a new plot window will be opened and `add = TRUE` will have no effect.
- **sample.size**: optionally specifies the size of a simple random sample to take before plotting. This can make the plot less computationally intensive.

#### Examples

```r
win1 <- CMBWindow(theta = c(0, pi/2, pi/2), phi = c(0, 0, pi/2))
win2 <- CMBWindow(theta = c(2*pi/3, 3*pi/4, 3*pi/4, 2*pi/3), phi = c(pi/4, pi/4, pi/3, pi/3))
plot(win1)
plot(win2)
```
type a single character indicating the type of item to plot. Supported types are: ‘p’ for points, ‘s’ for spheres, ‘l’ for lines, ‘h’ for line segments from $z = 0$, and ‘n’ for nothing.

size the size of plotted points

box whether to draw a box

axes whether to draw axes

aspect either a logical indicating whether to adjust the aspect ratio, or a new ratio.

col specify the colour(s) of the plotted points

back.col optionally specifies the background colour of the plot. This argument is passed to rgl::bg3d.

labels optionally specify a vector of labels to plot, such as words or vertex indices. If this is specified then rgl::text3d is used instead of rgl::plot3d. Then length(labels) must equal nrow(x)

hp.boundaries integer. If greater than 0 then HEALPix pixel boundaries at nside = hp.boundaries will be added to the plot

hpb.col colour for the hp.boundaries

depth_test The depth test to be applied to the plotted points. This controls how resistant the plotted object is to being obscured. This controls how resistant the plotted

lab_depth_test The rgl depth test to be applied to the labels and pixel boundaries if present. See rgl.material

... arguments passed to rgl::plot3d

Value

A plot of the data locations according to coordinate columns or HEALPix index

Examples

hpdf <- HPDataFrame(I = rep(0,12), nside = 1)
plot(hpdf, size = 5, col = “yellow”, back.col = “black”,
     hp.boundaries = 1)

plot.variogram Plot sample variogram

Description

Plots sample (empirical) variogram. Uses plot.variogram from geoR package.

Arguments

x An object of class variogram.

... Extra arguments as in plot.variogram passed to plot.default.
plotAngDis

Plot angular scatterplots and means

Description

For specified measurements from CMBDataFrame this function produces scatterplots and binned means versus theta and phi angles.

Usage

plotAngDis(cmbdf, intensities = "I")

Arguments

cmbdf A CMBDataFrame object.
intensities The name of a column of cmbdf, containing measured values.

Value

2x2 plot. The first row shows scatterplots. The second row gives barplots of the corresponding means computed over bins. The first column corresponds to the values of theta and the second one is for psi.
Examples

## Download the map first
# downloadCMBMap(foreground = "smica", nside = 1024)
# df <- CMBDataFrame("CMB_map_smica1024.fits")
# df.sample <- CMBDataFrame(df, sample.size = 80000)
# win <- CMBWindow(theta = c(pi/4, pi/2, pi/2, pi/4), phi = c(0, 0, pi/2, pi/2))
# cmbdf.win <- window(df.sample, new.window = win)
#
# intensities <- "I"
# plotAngDis(cmbdf.win, intensities)

plotcovmodelCMB  
Plot theoretical CMB Covariance

Description

Plots theoretical covariance functions from the list defined in covmodelCMB

Usage

plotcovmodelCMB(cov.model = "matern", sigmasq = 1, phi = pi, kappa = 0.5, from = 0, to = pi, ...)

Arguments

cov.model A type of the correlation function. Available choices are: "matern", "exponential", "spherical", "powered.exponential", "cauchy", "gencauchy", "pure.nugget", "askey", "c2wendland", "c4wendland", "sinepower", "multiquadric". The default is "matern"

sigmasq The variance parameter as documented in covmodelCMB. The default is 1.

phi The range parameter as documented in covmodelCMB. The default is pi.

kappa A smoothness parameter of the correlation function. The default is 0.5.

from A lower range of the plotting region. The default is lb = 0

to An upper range of the plotting region. The default is ub = pi.

Value

Produces a plot with the theoretical covariance function.

References

covmodelCMB
Examples

```r
plotcovmodelCMB("matern", sigmasq = 5)
plotcovmodelCMB("askey", phi = pi/4, to = pi/2, kappa = 4)
```

---

**plotvariogram**  
*Plot theoretical variogram*

---

**Description**

Plots theoretical variogram functions from the list defined in `covmodelCMB`

**Usage**

```r
plotvariogram(cov.model = "matern", sigmasq = 1, phi = pi,
              kappa = 0.5, from = 0, to = pi, ...)
```

**Arguments**

- `cov.model` A type of the variogram function. Available choices are: "matern", "exponential", "spherical", "powered.exponential", "cauchy", "gencauchy", "pure.nugget", "askey", "c2wendland", "c4wendland", "sinepower", "multiquadric". The default is "matern"
- `sigmasq` The variance parameter as documented in `covmodelCMB`. The default is 1.
- `phi` The range parameter as documented in `covmodelCMB`. The default is pi.
- `kappa` A smoothness parameter of the variogram function. The default is 0.5.
- `from` A lower range of the plotting region. The default is \(lb = 0\)
- `to` An upper range of the plotting region. The default is \(ub = \pi\).
- `...` optional plotting parameters.

**Value**

Produces a plot with the theoretical variogram.

**References**

`covmodelCMB`

**Examples**

```r
plotvariogram("matern", sigmasq = 5)
plotvariogram("askey", phi = pi/4, to = pi/2, kappa = 4)
```
practicalRangeCMB

Description

This function computes the practical range for covariance functions on spheres. The function extends `practicalRange` from the package `geoR` to additional covariance models on spheres.

Usage

```r
practicalRangeCMB(cov.model, phi, kappa = 0.5, correlation = 0.05, ...)
```

Arguments

- `phi`: The range parameter as documented in `covmodelCMB`
- `kappa`: A smoothness parameter of the correlation function.
- `correlation`: A correlation threshold (default is 0.05)
- `...`: other optimisation parameters

Details

The practical(effective) range for a covariance function is the distance at which a covariance function first time reaches the specified value `correlation`. For covariance functions on spheres the practical range does not exceed \( \pi \), the distance beyond which a covariance function is not defined. For the covariance functions "spherical", "askey", "c2wendland", "c4wendland" their practical ranges are equal to lengths of their support.

Value

Value of the practical range for the covariance function specified in `covmodelCMB`

References

- `geoR` package, `practicalRange`, `covmodelCMB`

Examples

```r
practicalRangeCMB(cov.model = "sinepower", phi = 0.1, kappa = 0.5)
practicalRangeCMB(cov.model = "askey", phi = 0.1, kappa = 0.5)
```
print.CMBDataFrame  

Print CMBDataFrame

Description
This function neatly prints the contents of a CMBDataFrame.

Usage
## S3 method for class 'CMBDataFrame'
print(x, ...)

Arguments

x  
A CMBDataFrame.

...  
arguments passed to print.tbl_df

Value
Prints contents of the CMB data frame to the console.

Examples
## First download the map
# downloadCMBMap(foreground = "smica", nside = 1024)
# df <- CMBDataFrame("CMB_map_smica1024.fits")
# print(df)

print.HPDataFrame  

Print a HPDataFrame

Description
This function neatly prints the contents of a HPDataFrame.

Usage
## S3 method for class 'HPDataFrame'
print(x, ...)

Arguments

x  
A HPDataFrame.

...  
arguments passed to print.tbl_df
**pwSpCorr**

**Value**

Prints contents of the HPDataFrame to the console.

**Examples**

```r
df <- HPDataFrame(I = rep(0,12), nside = 1, ordering = "nested")
print(df)
df
```

---

**pwSpCorr**  
*Power spectra estimate via correlation*

**Description**

This function provides an angular power spectra estimate using the values of the sample correlations. The approach is based on Lawson-Hanson algorithm for non-negative least squares.

**Usage**

```r
pwSpCorr(corcmb, lmax = 20 * length(corcmb$u))
```

**Arguments**

- `corcmb` An object of the class CMBCorrelation.
- `lmax` A number of angular power spectra components to estimate

**Value**

A data frame which first column is 1-d grid of l values from 0 to `lmax`. The second column is estimated angular power spectra components on this grid.

**References**


**Examples**

```r
## Download the map first
# downloadCMBMap(foreground = "smica", nside = 1024)
# df <- CMBDataFrame("CMB_map_smica1024.fits")
# Corrf <- corrCMB(df, max.dist = 0.1, num.bins = 30,
# sample.size=10000)
# pw <- pwSpCorr(Corrf)
```
Description

This function is a modification of standard "qqnorm" functions to work with "CMBWindow" regions.

Usage

`qqnormWin(cmbdf, win, intensities = "I")`

Arguments

cmbdf A CMBDataFrame.
win A CMBWindow
intensities A CMBDataFrame column with measured values.

Details

`qqnormWin` returns a normal QQ plot of for the specified CMBDataFrame column intensities and CMBWindow region. The function automatically adds a line of a “theoretical” normal quantile-quantile plot.

Value

A list with quantile components x and y and a normal QQ plot with QQ line

References

`qqnorm`, `qqplot`, `qqplotWin`

Examples

```r
## Download the map first
# downloadCMBMap(foreground = "smica", nside = 1024)
# df <- CMBDataFrame("CMB_map_smica1024.fits")
# cmbdf <- sampleCMB(df, sample.size = 1000)

# win1 <- CMBWindow(theta = c(0,pi/2,pi/2), phi = c(0,0,pi/2))
# qqnormWin(cmbdf, win1)
```
Description

This function is a modification of standard qqplot functions to work with CMBWindow regions.

Usage

```r
qqplotWin(cmbdf, win1, win2, intensities = "I")
```

Arguments

- `cmbdf`: A CMBDataFrame.
- `win1`: A CMBWindow.
- `win2`: A CMBWindow.
- `intensities`: A CMBDataFrame column with measured values.

Details

`qqplotWin` produces a QQ plot of quantiles of observations in two CMBWindows against each other for the specified CMBDataFrame column intensities. The function automatically adds a diagonal line.

Value

A list with quantile components x and y and a QQ plot with a diagonal line.

References

- `qqnormWin`, `qqnorm`, `qqplot`

Examples

```r
# Download the map first
# downloadCMBMap(foreground = "smica", nside = 1024)
# df <- CMBDataFrame("CMB_map_smica1024.fits")
# cmbdf <- sampleCMB(df, sample.size = 10000)

# win1 <- CMBWindow(theta = c(0,pi/2,pi/2), phi = c(0,0,pi/2))
# win2 <- CMBWindow(theta = c(2*pi/3,3*pi/4,3*pi/4, 2*pi/3),
#                  phi = c(pi/4,pi/4,pi/3,pi/3))

# qqplotWin(cmbdf, win1, win2)
```
Description

This function returns an estimated q-statistic for the specified column intensities in a CMBDataFrame and the list of CMBWindows.

Usage

qstat(cmbdf, listwin, intensities = "I")

Arguments

cmbdf  A CMBDataFrame.
listwin A list of CMBWindows
intensities A CMBDataFrame column with measured values.

Details

The q-statistics is used to measure spatial stratified heterogeneity and takes values in [0, 1]. It gives the percent of the variance of intensities explained by the stratification. 0 corresponds to no spatial stratified heterogeneity, 1 to perfect spatial stratified heterogeneity.

Value

Estimated q-statistics for observations in a list of CMBWindows

References


Examples

```r
## Download the map first
# downloadCMBMap(foreground = "smica", nside = 1024)
# df <- CMBDataFrame("CMB_map_smica1024.fits")
# cmbdf <- sampleCMB(df, sample.size = 1000)
# win1 <- CMBWindow(theta = c(0, pi/2, pi/2), phi = c(0, 0, pi/2))
# win2 <- CMBWindow(theta = c(pi/2, pi, pi/2), phi = c(0, 0, pi/2))
# lw <- list(win1, win2)
# qstat(cmbdf, lw)
```
Description

Add a new row or rows to a \texttt{CMBDataFrame}. All arguments passed to \ldots must be \texttt{CMBDataFrames}. If the \texttt{CMBDataFrame} arguments have overlapping pixel indices then all but one of the non-unique rows will be deleted unless unsafe = TRUE. If unsafe = TRUE then a \texttt{HPDataFrame} will be returned instead of a \texttt{CMBDataFrame}.

Usage

\begin{verbatim}
## S3 method for class 'CMBDataFrame'
rbind(\ldots, deparse.level = 1, unsafe = FALSE)
\end{verbatim}

Arguments

\begin{itemize}
\item \ldots A number of \texttt{CMBDataFrames}
\item deparse.level See documentation for \texttt{rbind.data.frame}.
\item unsafe A boolean. If the \texttt{CMBDataFrame} arguments have overlapping pixel indices then all but one of the non-unique rows will be deleted unless unsafe = TRUE. If unsafe = TRUE then a \texttt{HPDataFrame} will be returned instead of a \texttt{CMBDataFrame}.
\end{itemize}

See Also

See the documentation for \texttt{rbind}

Examples

\begin{verbatim}
df <- CMBDataFrame(nside = 1, I = 1:12)
df.123 <- CMBDataFrame(df, spix = c(1,2,3))
df.123
df.234 <- CMBDataFrame(df, spix = c(2,3,4))
df.234
df.1234 <- rbind(df.123, df.234)
df.1234
class(df.1234) # A CMBDataFrame
pix(df.1234)
df.123234 <- rbind(df.123, df.234, unsafe = TRUE)
df.123234
class(df.123234) # A HPDataFrame
pix(df.123234)
\end{verbatim}
Description

Handling and Analysing Spherical, Healpix and Cosmic Microwave Background data on a HEALPix grid.

Details

The package \texttt{rcosmo} offers various tools for

- Downloading and transforming Cosmic Microwave Background radiation (CMB) and spherical data
- Working with Hierarchical Equal Area isoLatitude Pixelation of a sphere (Healpix)
- Spherical geometry
- Statistical analysis of CMB and spherical data
- Visualisation of Healpix data

Most of \texttt{rcosmo} features were developed for CMB, but it can also be used for other spherical data. It contains tools for transforming spherical data in cartesian and geographic coordinates to the Healpix representation.

Update

Current updates are available through URL: https://github.com/frycast/rcosmo

BugReports

https://github.com/frycast/rcosmo/issues

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resolution

Get the arcmin resolution from a CMBDataFrame

Description

Get the arcmin resolution from a CMBDataFrame

Usage

resolution(cmbdf)

Arguments

cmbdf a CMBDataFrame.

Value

The arcmin resolution as specified by the FITS file where the data was sourced

Examples

## First download the map
# downloadCMBMap(foreground = "smica", nside = 1024)
# df <- CMBDataFrame("CMB_map_smica1024.fits")
# resolution(df)

ring2nest

Convert ring to nest ordering.

Description

ring2nest converts HEALPix pixel indices in the 'ring' ordering scheme to HEALPix pixel indices in the 'nested' ordering scheme.

Usage

ring2nest(nside, pix)

Arguments

nside is the HEALPix nside parameter (integer number $2^k$)
pix is a vector of HEALPix pixel indices, in the 'ring' ordering scheme.
Value

the output is a vector of HEALPix pixel indices in the ‘nested’ ordering scheme.

Examples

```r
## Convert (1,2,23) from ring to nest at nside = 8
nside <- 8
pix <- c(1,2,23)
ring2nest(nside, pix)
```

---

**sampleCMB**

Take a simple random sample from a CMBDataFrame

Description

This function returns a CMBDataFrame which size equals to sample.size, whose rows comprise a simple random sample of the rows from the input CMBDataFrame.

Usage

```r
sampleCMB(cmbdf, sample.size)
```

Arguments

- `cmbdf`: a CMBDataFrame.
- `sample.size`: the desired sample size.

Value

A CMBDataFrame which size equals to sample.size, whose rows comprise a simple random sample of the rows from the input CMBDataFrame.

Examples

```r
## Download the map first
# downloadCMBMap(foreground = "smica", nside = 1024)
# df <- CMBDataFrame("CMB_map_smica1024.fits")
# plot(sampleCMB(df, sample.size = 800000))

df <- CMBDataFrame(nside = 16, I = rnorm(12 * 16 ^ 2), ordering = "nested")
df.sample <- sampleCMB(df, sample.size = 100)
df.sample
```
siblings

Return siblings of pixel

Description
The siblings of pixel p are defined as the children of the parent of p. Note this is resolution independent.

Usage
siblings(p)

Arguments
p Pixel index in nested order.

Examples
siblings(11)
siblings(12)

sphericalHarmonics
Compute spherical harmonic values at given points on the sphere.

Description
The function sphericalHarmonics computes the spherical harmonic values for the given 3D Cartesian coordinates.

Usage
sphericalHarmonics(L, m, xyz)

Arguments
L The degree of spherical harmonic (L=0,1,2,...)
m The order number of the degree-L spherical harmonic (m=-L,-L+1,...,L-1,L)
xyz Dataframe for given points in 3D cartesian coordinates

Value
values of spherical harmonics
References

See https://en.wikipedia.org/wiki/Table_of_spherical_harmonics

It uses equation (7) in Hesse, K., Sloan, I. H., & Womersley, R. S. (2010). Numerical integration on the sphere. In Handbook of Geomathematics (pp. 1185-1219). Springer Berlin Heidelberg, but instead of the order $k=1,...,2L+1$ in the book we use $m=k-L-1$.

Examples

```r
### Calculate spherical harmonic value at
### the point $(0,1,0)$ with $L=5$, $m=2$
point<-data.frame(x=0,y=1,z=0)
sphericalHarmonics(5,2,point)

### Calculate spherical harmonic values at
### the point $(1,0,0)$, $(0,1,0)$, $(0,0,1)$ with $L=5$, $m=2$
points<-data.frame(diag(3))
sphericalHarmonics(5,2,points)
```

summary.CMBDataFrame  Summarise a CMBDataFrame

Description

This function produces a summary from a CMBDataFrame.

Usage

```r
## S3 method for class 'CMBDataFrame'
summary(object, intensities = "I", ...)
```

Arguments

- **object**: A `CMBDataFrame`.
- **intensities**: the name of a column specifying CMB intensities (or potentially another numeric quantity of interest)
- **...**: Unused arguments.

Value

A summary includes window’s type and area, total area covered by observations, and main statistics for intensity values
Examples

## First download the map

```r
# downloadCMBMap(foreground = "smica", nside = 1024)
# df <- CMBDataFrame("CMB_map_smica1024.fits")
# df.sample <- CMBDataFrame(df, sample.size = 800000)
# summary(df.sample)
```

```r/ns <- 16
df <- CMBDataFrame(I = rnorm(12*ns^2), nside = ns,
                   ordering = "nested")
```

```r
win1 <- CMBWindow(x=0,y=3/5,z=4/5,r=0.8)
df.sample1 <- window(df, new.window = win1)
```

```r
summary(df)
```

---

**summary.CMBWindow**

*Summarise a CMBWindow*

**Description**

This function produces a summary from a CMBWindow

**Usage**

```r
## S3 method for class 'CMBWindow'
summary(object, ...)
```

**Arguments**

- `object` A CMBWindow.
- `...` Unused arguments.

**Value**

A summary includes window's type and area

**Examples**

```r
win <- CMBWindow(theta = c(0,pi/2,pi/2), phi = c(0,0,pi/2))
summary(win)
```

```r
win1<- CMBWindow(x=0,y=3/5,z=4/5,r=0.8, set.minus = TRUE)
summary(win1)
```
summary.HPDataFrame  

**Summarise a HPDataFrame**

**Description**

This function produces a summary from a HPDataFrame.

**Usage**

```r
## S3 method for class 'HPDataFrame'
summary(object, intensities = "I", ...)
```

**Arguments**

- `object`: A HPDataframe.
- `intensities`: the name of a column specifying intensities (or potentially another numeric quantity of interest)
- `...`: Unused arguments.

**Value**

A summary includes window’s type and area, total area covered by observations, and main statistics for intensity values.

**Examples**

```r
ns <- 2
hpdf <- HPDataFrame(I = rnorm(12*ns^2), nside = 2, ordering = "nested")
win <- CMBWindow(theta = c(0,pi/2,pi/2), phi = c(0,0,pi/2))
hpdf.win <- window(hpdf, new.window = win)
summary(hpdf.win)
```

---

triangulate  

**Triangulate a polygonal CMBWindow**

**Description**

Triangulate a polygonal CMBWindow

**Usage**

```r
triangulate(win)
```
Arguments

win a CMBWindow object

Value

a list of CMBWindow polygons or minus.polygons, each having 3 vertices and representing a triangle. If winType of win does not include "minus" then these triangles have pairwise disjoint interiors and their union is equal to the original polygon, win. Otherwise, if winType of win does include "minus" the triangles are the same as for the non-minus type above, but have "minus" types.

Examples

```r
## Example 1
win <- CMBWindow(theta = c(2* pi / 3, 3* pi / 4, 3* pi / 4, 2* pi / 3),
                 phi = c( pi / 4, pi / 4, pi / 3, pi / 3))
win
plot(win)
win1 <- triangulate(win)
summary(win1[[1]])
plot(win1[[1]], add = FALSE, col = "green")
plot(win1[[2]], col = "blue")

## Example 2: triangulation minus-type polygon
win <- CMBWindow(theta = c(pi / 5, pi / 3, pi / 4, pi / 3, pi / 5),
                 phi = c(pi / 5, pi / 5, pi / 4, pi / 3, pi / 3), set.minus = TRUE)
win
plot(win)
summary(win)
win1 <- triangulate(win)
summary(win1[[1]])
plot(win1[[1]], add = FALSE, col = "green")
plot(win1[[2]], col = "blue")
plot(win1[[3]], col = "yellow")
summary(win1[[1]])
summary(win1[[2]])
summary(win1[[3]])
```

variofitCMB Estimates parameters of variograms

Description

This function estimates variogram parameters by fitting a parametric model from covmodelCMB to a sample variogram. The function extends variofit from the package geoR to additional covariance models on spheres.
Usage

dechofitCMB(vario, ini.cov.pars, cov.model, fix.nugget = FALSE,
nugget = 0, fix.kappa = TRUE, kappa = 0.5, simul.number = NULL,
max.dist = vario$max.dist, weights, minimisation.function,
limits = geoR::pars.limits(), messages, ...)

Arguments

vario An object of the class variogram obtained as an output of the function dechofitCMB.
ini.cov.pars A vector with initial values for the variogram parameters. The first parameter corresponds to the variance sigma^2. The second parameter corresponds to the range phi of the correlation function.
cov.model A type of the variogram function. Available choices are: "matern", "exponential", "spherical", "powered.exponential", "cauchy", "gencauchy", "pure.nugget", "askey", "c2wendland", "c4wendland", "sinepower", "multiquadric". The default is "matern"
fix.nugget logical. Indicates whether the nugget variance should be regarded as fixed or be estimated. The default is FALSE.
nugget A value for the nugget parameter. Regarded as a fixed values if fix.nugget = TRUE or as a initial value for the minimization algorithm if fix.nugget = FALSE. The default is zero.
fix.kappa logical. Indicates whether the parameter kappa should be regarded as fixed or be estimated. The default is TRUE.
kappa A value for the smoothness parameter. Regarded as a fixed values if fix.kappa = TRUE or as a initial value for the minimization algorithm if fix.kappa = FALSE. Required not in all covariance models, see dcovsahodelCMB. The default is 0.5.
simul.number number of simulation. Used if vario has empirical variograms for more than one data-set (simulations). The default is NULL
max.dist A maximum distance to fit a variogram model. The default is x$max.dist.
weights Weights used in the loss function in the minimization algorithm.
minimisation.function Minimization function ("optim", "nlm", "nls") to estimate the parameters.
limits Lower and upper limits for the model parameters used in the numerical minimisation by minimisation.function = "optim".
messages logical. Indicates whether or not status messages are printed on the screen.
... other minimisation parameters

Details

The parameter values of a variogram function from dcovsahodelCMB are found by numerical optimization using one of the functions: optim, nlm and nls.

The function extends dechofit from the package geoR to additional variogram models on spheres. Available models are: "matern", "exponential", "spherical", "powered.exponential", "cauchy", "gencauchy", "pure.nugget", "askey", "c2wendland", "c4wendland", "sinepower", "multiquadric".
Additionally it rescales an empirical variogram to the range \([0,1]\) before numerical optimisation and then transforms all obtained results to the original scale. If ini.cov.pars are not provided then the 5x5 grid \((\text{seq}(0,\max(vario$v),l=5),\text{seq}(0,\max(vario$max.dist),l=5))\) of initial values of \(\sigma^2\) and \(\phi\) is used.

**Value**

An object of the class variomodel and variofit, see `variofit`.

**References**

`geoR` package, `variofit`, `covmodelCMB`.

**Examples**

```r
# df <- CMBDataFrame("../CMB_map_smica1024.fits")
# cmbdf <- sampleCMB(df, sample.size = 10000)
# varcmb <- variogramCMB(cmbdf, max.dist = 0.1, num.bins = 30)
# varcmb
#
# ols <- variofitCMB(varcmb, fix.nug=FALSE, wei="equal", cov.model = "matern")
# plot(varcmb)
# lines(ols, lty=2)
# str(ols)
#
# ols <- variofitCMB(varcmb, fix.nug = TRUE, kappa = 3, wei = "equal",
# cov.model = "askey")
# plot(varcmb, main = ols$cov.model)
# linesCMB(ols, lty = 2)
# str(ols)
```

---

### variogramCMB

**Sample variogram**

**Description**

This function provides an empirical variogram for data in a `CMBDataFrame` or data.frame. It assumes that data are from a stationary spherical random field and the covariance depends only on a geodesic distance between locations. Output is a binned variogram.

**Usage**

```r
variogramCMB(cmbdf, num.bins = 10, sample.size, max.dist = pi, breaks, 
equiareal = TRUE, calc.max.dist = FALSE)
```
Arguments

cmbdf is a CMDBDataFrame or data.frame
num.bins specifies the number of bins
sample.size optionally specify the size of a simple random sample to take before calculating variogram. This may be useful if the full covariance computation is too slow.
max.dist an optional number between 0 and pi specifying the maximum geodesic distance to use for calculating covariance. Only used if breaks are unspecified.
breaks optionally specify the breaks manually using a vector giving the break points between cells. This vector has length num.bins since the last break point is taken as max.dist. If equiareal = TRUE then these breaks should be \( \cos(r_i) \) where \( r_i \) are radii. If equiareal = FALSE then these breaks should be \( r_i \).
equiareal if TRUE then the bins have equal spherical area. If false then the bins have equal annular widths. Default is TRUE.
calc.max.dist if TRUE then the max.dist will be calculated from the locations in cmbdf. Otherwise either max.dist must be specified or max.dist will default to pi.

Value

An object of class variog specified in the package geoR.
The attribute "breaks" contains the break points used to create bins. The result has num.bins + 1 values since the first value at distance 0 is not counted as a bin.

- \( u \) a vector with distances.
- \( v \) a vector with estimated variogram values at distances given in \( u \).
- \( n \) number of pairs in each bin
- \( sd \) standard deviation of the values in each bin
- \( bins.lim \) limits defining the interval spanned by each bin
- \( ind.bin \) a logical vector indicating whether the number of pairs in each bin is greater or equal to the value in the argument pairs.min
- \( var.mark \) variance of the data
- \( beta.ols \) parameters of the mean part of the model fitted by ordinary least squares
- \( output.type \) echoes the option argument
- \( max.dist \) maximum distance between pairs allowed in the variogram calculations
- \( n.data \) number of data
- \( direction \) direction for which the variogram was computed
- \( call \) the function call

References

geoR package, variog.covCMB, corrCMB
## Examples

```r
## Download the map first
# downloadCMBMap(foreground = "smica", nside = 1024)
# df <- CMBDataFrame("CMB_map_smica1024.fits")
# cmbdf <- sampleCMB(df, sample.size = 100000)
# varcmb <- variogramCMB(cmbdf, max.dist = 0.1, num.bins = 30, sample.size=100)
# varcmb
```

---

### Description

Detailed descriptions and examples can be found in documentation for specific window functions `window.CMBDataFrame`, `window.HPDataFrame`, `window.data.frame`

### Usage

```r
window(x, ...)
```

### Arguments

- `x`: An object.
- `...`: Extra arguments.

### See Also

- `window.CMBDataFrame`  
- `window.HPDataFrame`  
- `window.data.frame`

---

### window.CMBDat

*Get a sub window from a CMBDat object*

### Description

This function returns a data.frame containing the data in *x* restricted to the CMBWindow *new.window*.

### Usage

```r
## S3 method for class 'CMBDat'
window(x, new.window, intersect = TRUE, ...)
```
Arguments

x       a CMBDat object.
new.window       A single CMBWindow object or a list of them.
intersect       A boolean that determines the behaviour when new.window is a list containing BOTH regular type and "minus" type windows together (see details).
...       Unused arguments.

Details

Windows that are tagged with set.minus (see CMBWindow) are treated differently from other windows.

If the argument is a list of CMBWindows, then interiories of all windows whose winType does not include "minus" are united (let A be their union) and exteriors of all windows whose winType does include "minus" are intersected, (let B be their intersection). Then, provided that intersect = TRUE (the default), the returned data.frame will be the points of cmbdat$data in the the intersection of A and B. Otherwise, if intersect = FALSE, the returned data.frame consists of the points of x$data in the union of A and B.

Note that if A (resp. B) is empty then the returned data.frame will be the points of x in B (resp. A).

Value

A CMBDataFrame containing the data in x restricted to the CMBWindow new.window

Examples

win1 <- CMBWindow(theta = c(0,pi/2,pi/2), phi = c(0,0,pi/2))

## Ensure you have a FITS file with correct path
## before uncommenting and running the rest of the example:
# cmbdat <- CMBDat("CMB_map_smica1024.fits", mmap = TRUE)
# class(cmbdat)
# cmbdat.win <- window(cmbdat, new.window = win1)
# class(cmbdat.win)
Usage

```r
## S3 method for class 'CMBDataFrame'
window(x, new.window, intersect = TRUE, in.pixels,
in.pixels.res = 0, ...)
```

Arguments

- `x`: A `CMBDataFrame`.
- `new.window`: Optionally specify a new window in which case a new `CMBDataFrame` is returned whose `CMBWindow` is `new.window`. `new.window` may also be a list (see details section and examples).
- `intersect`: A boolean that determines the behaviour when `new.window` is a list containing BOTH regular type and "minus" type windows together (see details).
- `in.pixels`: A vector of pixels at resolution `in.pixels.res` whose union contains the window(s) `new.window` entirely, or if `new.window` is unspecified then this whole pixel is returned.
- `in.pixels.res`: An integer. Resolution (i.e., $j$ such that nside $= 2^j$) at which the `in.pixels` parameter is specified
- `...`: Unused arguments.

Details

Windows that are tagged with `set.minus` (see `CMBWindow`) are treated differently from other windows.

If the argument `new.window` is a list of `CMBWindows`, then interios of all windows whose win-Type does not include "minus" are united (let $A$ be their union) and exteriors of all windows whose winType does include "minus" are intersected, (let $B$ be their intersection). Then, provided that `intersect = TRUE` (the default), the returned `CMBDataFrame` will be the points of cmbdf in the the intersection of $A$ and $B$. Otherwise, if `intersect = FALSE`, the returned `CMBDataFrame` consists of the points of $x$ in the union of $A$ and $B$.

Note that if $A$ (resp. $B$) is empty then the returned `CMBDataFrame` will be the points of $x$ in $B$ (resp. $A$).

Value

The window attribute of $x$ or, if `new.window/in.pixels` is specified, a new `CMBDataFrame`.

Examples

```r
## Example 1: Create a new CMBDataFrame with a window

cmbdf <- CMBDataFrame(nside = 64, coords = "cartesian",
                      ordering = "nested")
win <- CMBWindow(theta = c(0,pi/2,pi/2), phi = c(0,0,pi/2))
cmbdf.win <- window(cmbdf, new.window = win)
```
## Example 2: Change the window of an existing CMBDataFrame

cmbdf <- CMBDataFrame(nside = 64, coords = "cartesian", ordering = "nested")
window(cmbdf) <- win2 <- CMBWindow(theta = c(pi/6, pi/3, pi/3, pi/6),
phi = c(0, 0, pi/6, pi/6))
plot(cmbdf)

## Example 3: union of windows

## Create 2 windows
win1 <- CMBWindow(theta = c(0, pi/2, pi/2), phi = c(0, 0, pi/2))
win2 <- CMBWindow(theta = c(2*pi/3, 3*pi/4, 3*pi/4, 2*pi/3),
phi = c(pi/4, pi/4, pi/3, pi/3))
plot(win1)
plot(win2)

## Create CMBDataFrame with points in the union of win1 and win2

cmbdf <- CMBDataFrame(nside = 64, coords = "cartesian", ordering = "nested")
cmbdf.win <- window(cmbdf, new.window = list(win1, win2), intersect = FALSE)
plot(cmbdf.win)

## Example 4: intersection of windows

## Create 2 windows
win1 <- CMBWindow(theta = c(0, pi/2, pi/2), phi = c(0, 0, pi/2))
win2 <- CMBWindow(theta = c(pi/4, pi/3, pi/3, pi/4),
phi = c(pi/4, pi/4, pi/3, pi/3))
plot(win1)
plot(win2)

## Create CMBDataFrame with points in the intersection of win1 and win2

cmbdf <- CMBDataFrame(nside = 64, coords = "cartesian", ordering = "nested")
cmbdf.win1 <- window(cmbdf, new.window = win1)
cmbdf.win12 <- window(cmbdf.win1, new.window = win2)
plot(cmbdf.win12)
plot(win1)
plot(win2)

## Example 5: intersection of windows with "minus" type

## Create 2 windows with "minus" type
win1 <- CMBWindow(theta = c(0, pi/2, pi/2), phi = c(0, 0, pi/2),
set.minus = TRUE)
win2 <- CMBWindow(theta = c(pi/4, pi/3, pi/3, pi/4),
phi = c(pi/4, pi/4, pi/3, pi/3),
set.minus = TRUE)
plot(win1)
plot(win2)

## Create CMBDataFrame with points in the intersection of win1 and win2

cmbdf <- CMBDataFrame(nside = 64, coords = "cartesian", ordering = "nested")
cmbdf.win <- window(cmbdf, new.window = list(win1, win2))
plot(cmbdf.win)

## Example 6: intersection of windows with different types

## Create 2 windows, one with "minus" type

win1 <- CMBWindow(theta = c(0, pi/2, pi/2), phi = c(0, 0, pi/2))
win2 <- CMBWindow(theta = c(pi/4, pi/3, pi/3, pi/4),
phi = c(pi/4, pi/4, pi/3, pi/4),
set.minus = TRUE)
plot(win1)
plot(win2)

cmbdf <- CMBDataFrame(nside = 64, coords = "cartesian", ordering = "nested")
cmbdf.win <- window(cmbdf, new.window = list(win1, win2), intersect = TRUE)
plot(cmbdf.win)

## Example 7: union of windows with different types

win1 <- CMBWindow(theta = c(0, pi/2, pi/2), phi = c(0, 0, pi/2), set.minus = TRUE)
win2 <- CMBWindow(theta = c(pi/4, pi/3, pi/3, pi/4), phi = c(pi/4, pi/4, pi/3, pi/3))
plot(win1)
plot(win2)

cmbdf <- CMBDataFrame(nside = 64, coords = "cartesian", ordering = "nested")
cmbdf.win <- window(cmbdf, new.window = list(win1, win2), intersect = FALSE)
plot(cmbdf.win)

---

**window.data.frame**

*Get a sub window from a data.frame*

**Description**

This function returns a data.frame containing the data in `x` restricted to the CMBWindow `new.window`. 

Data frame containing the data in `x` restricted to the CMBWindow `new.window`.
Usage

## S3 method for class 'data.frame'
window(x, new.window, intersect = TRUE, ...)

Arguments

x
A data.frame. Must have columns labelled x,y,z specifying cartesian coordinates, or columns labelled theta, phi specifying colatitude and longitude respectively.

new.window
A single CMBWindow object or a list of them.

intersect
A boolean that determines the behaviour when new.window is a list containing BOTH regular type and "minus" type windows together (see details).

...
Unused arguments.

Details

Windows that are tagged with set.minus (see CMBWindow) are treated differently from other windows.

If the argument is a list of CMBWindows, then interiors of all windows whose winType does not include "minus" are united (let \( A \) be their union) and exteriors of all windows whose winType does include "minus" are intersected, (let \( B \) be their intersection). Then, provided that intersect = TRUE (the default), the returned data.frame will be the points of \( x \) in the the intersection of \( A \) and \( B \). Otherwise, if intersect = FALSE, the returned data.frame consists of the points of \( x \) in the union of \( A \) and \( B \).

Note that if \( A \) (resp. \( B \)) is empty then the returned data.frame will be the points of \( x \) in \( B \) (resp. \( A \)).

Value

A data.frame containing the data in \( x \) restricted to the CMBWindow new.window

Examples

```r
win1 <- CMBWindow(theta = c(0,pi/2,pi/2), phi = c(0,0,pi/2))
cmbdf <- CMBDataFrame(nside = 4)
df2 <- coords(cmbdf, new.coords = "cartesian")
df <- as.data.frame(df2[,1:3])
df
df.win <- window(df, new.window = win1)
df.win
```
Get a sub window from a HPDataFrame

Description

This function returns a HPDataFrame containing the data in hpdf restricted to the CMBWindow new.window. If the HPDataFrame has columns x,y,z or theta, phi then these will be used to determine locations with priority over the HEALPix indices in pix(hpdf) unless healpixCentered = TRUE is given. Note that if healpixCentered = TRUE then columns x,y,z or theta, phi will be discarded and replaced with pixel center locations.

Usage

```r
## S3 method for class 'HPDataFrame'
window(x, new.window, intersect = TRUE,
       healpixCentered = FALSE, ...)
```

Arguments

- **x**: A HPDataFrame.
- **new.window**: Optional. A single CMBWindow object or a list of them.
- **intersect**: A boolean that determines the behaviour when new.window is a list containing BOTH regular type and "minus" type windows together (see details).
- **healpixCentered**: A boolean. If the HPDataFrame has columns x,y,z or theta, phi then these will be used to determine locations with priority over the HEALPix indices in pix(x) unless healpixCentered = TRUE is given. Note that if healpixCentered = TRUE then columns x,y,z or theta, phi will be discarded and replaced with pixel center locations.
- **...**: Unused arguments.

Details

Windows that are tagged with set.minus (see CMBWindow) are treated differently from other windows.

If the argument is a list of CMBWindows, then interiors of all windows whose winType does not include "minus" are united (let A be their union) and exteriors of all windows whose winType does include "minus" are intersected, (let B be their intersection). Then, provided that intersect = TRUE (the default), the returned data.frame will be the points of df in the the intersection of A and B. Otherwise, if intersect = FALSE, the returned data.frame consists of the points of df in the union of A and B.

Note that if A (resp. B) is empty then the returned data.frame will be the points of df in B (resp. A).
winType

Value

A HPDataFrame containing the data in x restricted to the CMBWindow new.window. Or, if new.window is unspecified, then the window attribute of x is returned instead (and may be NULL).

Examples

```r
ns <- 16
hpdf <- HPDataFrame(nside = ns, I = 1:(12*ns^2))
hpdf

win1 <- CMBWindow(theta = c(0,pi/2,pi/2), phi = c(0,0,pi/2))
plot(hpdf); plot(win1)

hpdf.win <- window(hpdf, new.window = win1)
plot(hpdf.win, col = "yellow", size = 4, add = TRUE)
attributes(hpdf.win)
window(hpdf.win)
hpdf.win
```

---

### Description

Get/change the winType (polygon or disk) of a CMBWindow. If new.type is missing then the `winType` of `win` is returned. Otherwise, a new window is returned with `winType` equal to new.type. If you want to change the `winType` of `win` directly, then use `winType<-`, see the examples below.

### Usage

```r
winType(win, new.type)
```

### Arguments

- **win**: a CMBWindow object or a list of such
- **new.type**: optionally specify a new type. Use this to change between "polygon" and "minus.polygon" or to change between "disc" and "minus.disc"

### Value

If new.type is missing then the `winType` of `win` is returned. Otherwise a new window is returned with `winType` equal to new.type
Examples

```r
win <- CMBWindow(theta = c(pi/2, pi/2, pi/3, pi/3), phi = c(0, pi/3, pi/3, 0))
winType(win)

win1 <- CMBWindow(x=0, y=3/5, z=4/5, r=0.8)
winType(win1)
cmbdf <- CMBDataFrame(nside = 64, coords = "cartesian",
                      ordering = "nested")
cmbdf.win1 <- window(cmbdf, new.window = win1)
plot(cmbdf.win1)

winType(win1) <- "minus.disc"
winType(win1)
cmbdf <- CMBDataFrame(nside = 64, coords = "cartesian",
                      ordering = "nested")
cmbdf.win1 <- window(cmbdf, new.window = win1)
plot(cmbdf.win1)
```
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